



INT. **STIC Search Report**

Biotech-Chem Library

STIC Database Tracking Number: 108250

TO: Elizabeth Kemmerer
Location: cm1/10b17/10d19
Art Unit: 1646
Sunday, November 16, 2003

Case Serial Number: 08/741095

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Kemmerer,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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WO96/34095

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:31:51 ; Search time 30 Seconds
 (without alignments)
 1722.144 Million cell updates/sec

Title: US-08-741-095B-26
 Perfect score: 1578
 Sequence: 1 MEEPGDWGPPPWRSTPRTDV.....VVTVVAEETIPSFTCRSPNH 283

Scoring table: BL0SUM62
 Scoring gap: Gapext 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : Published Applications AA,*

1: /cgmn_6/ptodata/1/pubbaa/PTCUTS_PUBCOMB.pep:*

2: /cgmn_6/ptodata/1/pubbaa/PCT_NNEW_PUB.pep:*

3: /cgmn_6/ptodata/1/pubbaa/US06_PUBCOMB.pep:*

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12: /cgmn_6/ptodata/1/pubbaa/US09_NNEW_PUB.pep:*

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15: /cgmn_6/ptodata/1/pubbaa/US10_NNEW_PUB.pep:*

16: /cgmn_6/ptodata/1/pubbaa/US60_PUBCOMB.pep:*

17: /cgmn_6/ptodata/1/pubbaa/US60_PUBCOMB.pep:*

18: /cgmn_6/ptodata/1/pubbaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
1	1578	100.0	283	10	US-09-924-231-2
2	1578	100.0	283	10	US-09-924-282A-13

; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB1098-061C1CN1(M)
; CURRENT APPLICATION NUMBER: US 09/1934, 289A
; CURRENT FILING DATE: 2001-08-21
; PRIORITY NUMBER: US 09/342, 767
; PRIORITY FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: US 09/146, 950
; PRIORITY FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 44
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-1934-289A-44

Query Match 73.0%: Score 1152.5: DB 10: Length 239;
Best Local Similarity 92.4%; Pred. No. 7.1e-90; Matches 207; Conservative 2; Mismatches 6; Indels 9; Gaps 1;

Qy 39 LPSCKEDEYPVSECCPKCKPSGPYGRVKACGELGTGVCEPCPCPGTYIAHNLGSKLQCOM 98
Db 1 LUSCKEDEYPVSECCPKCKPSGPYGRVKACGELGTGVCEPCPCPGTYIAHNLGSKLQCOM 60

Qy 99 CPDAMGLRASNRCSRTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVOKGGTESQ 158
Db 61 CPDAMGLRASNRCSRTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVOKGGTESQ 120

Qy 159 DTLQCONCPGCTSPNGTLEECOHOTKSWLVTKAAGTSSSHWWFLSGLIVIVCST 218
Db 121 DTLQCONCPGCTSPNGTLEECOHOTKSWLVTKAAGTSSSHWWFLSGLIVIVCST 180

Qy 219 VGLIICVKKRKKGPRGVKVKIVIVSORKHQEAEGBATVIAQAPP 262
Db 181 VGLIICVKKRKKGPRGVKVKIVIVSORKHQEAEGBATVIAQAPP 215

RESULT 8
US-09-924-231-7
; Sequence 7, Application US/09924231
; Patent No. US20020102644A1

; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-01
; CURRENT APPLICATION NUMBER: US/09/924, 231
; CURRENT FILING DATE: 2001-08-08
; PRIORITY NUMBER: US 09/333, 279
; PRIORITY FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 7
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-924-231-7

Query Match 67.7%: Score 1068: DB 10: Length 193;
Best Local Similarity 98.4%; Pred. No. 8.1e-83; Matches 184; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEPPGDWGPPIPWRSTPRTDVLRLVLYTFLGAPCYAAPALPSCKEDEYPVSECCPKCKSPG 60
Db 1 MEPPGDWGPPIPWRSTPRTDVLRLVLYTFLGAPCYAAPALPSCKEDEYPVSECCPKCKSPG 60

Qy 61 YRVKEACGELGTGVCEPCPCPGTYIAHNLGSKLQCOMCPAMGLRASNRCSRTENAVCG 120
Db 61 YRVKEACGELGTGVCEPCPCPGTYIAHNLGSKLQCOMCPAMGLRASNRCSRTENAVCG 120

Qy 121 CSPGHFCIVQGDHCAACRAYATSSPGQRVOKGGTESQDTLCQNCPFGTSPNGTLEECQ 180
Db 121 CSPGHFCIVQGDHCAACRAYATSSPGQRVOKGGTESQDTLCQNCPFGTSPNGTLEECQ 180

Qy 181 HOTKCSW 187
Db 181 HOTKCSW 187

RESULT 10
US-09-934-289A-18
; Sequence 18, Application US/09934289A
; Patent No. US20020132297A1

; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB1098-061C1CN1(M)
; CURRENT APPLICATION NUMBER: US 09/342, 289A
; CURRENT FILING DATE: 2001-08-21
; PRIORITY NUMBER: US 09/342, 767
; PRIORITY FILING DATE: 1998-06-29
; PRIORITY NUMBER: US 09/146, 950
; PRIORITY FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0

; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-020-787-2

Query Match Similarity 99.8%; Score 1575; DB 14; Length 283;
Best Local Similarity 99.6%; Pred. No. 1.4e-125; Mismatches 0; Indels 0; Gaps 0;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDWGPWRSTPRTDVLVLYLTFGACYAPALPSCKEDYPVGSECCPKCSPG 60
1 MEPPGDWGPWRSTPRTDVLVLYLTFGACYAPALPSCKEDYPVGSECCPKCSPG 60

QY 61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120
61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120

Db 61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120
CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180

QY 121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180
121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180

Db 121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180
HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240

Qy 181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240
181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240

Db 241 VORKRQEAEVATEVIALQAPPDVITVAETBETIPSTGRSPNH 283
241 VORKRQEAEVATEVIALQAPPDVITVAETBETIPSTGRSPNH 283

RESULT 5

US-10-066-209-2

; Sequence 2, Application US/10066209
; Publication No. US2002011511A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: GH-5000-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-10-066-209-2

Query Match Similarity 93.5%; Score 1373.5; DB 10; Length 277;
Best Local Similarity 93.0%; Pred. No. 1.6e-108; Mismatches 6; Indels 9; Gaps 1;
Matches 245; Conservative 2; Mismatches 6; Indels 9; Gaps 1;

QY 1 MEPPGDWGPWRSTPRTDVLVLYLTFGACYAPALPSCKEDYPVGSECCPKCSPG 60
1 MEPPGDWGPWRSTPRTDVLVLYLTFGACYAPALPSCKEDYPVGSECCPKCSPG 60

QY 61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120
61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120

Db 61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120
CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180

QY 121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180
121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180

Db 121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180
181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240

QY 181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240
181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240

Db 241 VORKRQEAEVATEVIALQAPPDVITVAETBETIPSTGRSPNH 262
241 VORKRQEAEVATEVIALQAPPDVITVAETBETIPSTGRSPNH 262

RESULT 6

US-09-934-289A-42

; Sequence 42, Application US/09934289A
; Patent No. US20030132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED PROTEIN FAMILY AND USES THEREOF
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB1098-001CP1EN1(M)
; CURRENT APPLICATION NUMBER: US/09/934, 289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146, 950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 277
; TYPE: PRT
; ORGANISM: HOMO sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(38)

US-09-934-289A-42

Query Match Similarity 87.0%; Score 1373.5; DB 10; Length 277;
Best Local Similarity 93.5%; Pred. No. 1.6e-108; Mismatches 6; Indels 9; Gaps 1;
Matches 245; Conservative 2; Mismatches 6; Indels 9; Gaps 1;

QY 1 MEPPGDWGPWRSTPRTDVLVLYLTFGACYAPALPSCKEDYPVGSECCPKCSPG 60
1 MEPPGDWGPWRSTPRTDVLVLYLTFGACYAPALPSCKEDYPVGSECCPKCSPG 60

QY 61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120
61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120

Db 61 YRVEACAGELTGTVCEPCPGTYIAHNGLSKLCQCMCDPAMGLRASRNCSRTENAVCG 120
CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180

QY 121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180
121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180

Db 121 CSPGHFCIVODGDHACRAYATSSPGQRVKGGTESQDTLCONCPGTFSPNGLTECQ 180
181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240

QY 181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240
181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVCSTVGLICVKRRXPRGDVVKIVS 240

Db 241 VORKRQEAEVATEVIALQAPPDVITVAETBETIPSTGRSPNH 253
241 VORKRQEAEVATEVIALQAPPDVITVAETBETIPSTGRSPNH 253

RESULT 7

US-09-934-289A-44

; Sequence 44, Application US/09934289A
; Patent No. US20030132297A1
; GENERAL INFORMATION:
; APPLICANT: Buffield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE

RESULT 14
US-09-934-289A-20
; Sequence 20, Application US/09934289A
; Patent No. US2002132297A1
; GENERAL INFORMATION:
; APPLICANT: Buffield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB109-061CPCN1(M)
; CURRENT APPLICATION NUMBER: US/09/934, 289A
; CURRENT FILING DATE: 2001-08-21
; PRIORITY NUMBER: US 09/342, 767
; PRIORITY FILING DATE: 1999-06-29
; PRIORITY APPLICATION NUMBER: US 09/146, 950
; PRIORITY FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 20
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-934-289A-20

Query Match 53.2%; Score 839; DB 10; Length 159;
Best Local Similarity 98.0%; Pred. No. 1.6e-63; Mismatches 0; Indels 2; Gaps 1;
Matches 146; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 39 LPSCKEDBYPVGSECCPKCSPGVRKBEAGELTGTVBPCPCTYAHNLGSKCLOCOM 98
Db 1 LSPCKEDBYPVGSECCPKCSPGVRKBEAGELTGTVBPCPCTYAHNLGSKCLOCOM 60

Qy 99 CDPAMGLRASRNCSRTENAVCGSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGETSQ 158
Db 61 CDPAMGLRASRNCSRTENAVCGSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGETSQ 120

Qy 159 DTLCQNCPGTTSPNGTIEBECQHQT K 184
Db 121 DTLCQNCPGTTSPNGTIEBECQHQT K 146

RESULT 15
US-10-247-671-152
; Sequence 152, Application US/10247671
; Publication No. US200310194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Schiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kasey, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247, 671
; CURRENT FILING DATE: 2002-03-18
; PRIORITY NUMBER: 60/323, 784
; PRIORITY FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL program
; SEQ ID NO 152

Query Match 17.0%; Score 268.5; DB 12; Length 277;
Best Local Similarity 26.1%; Pred. No. 6.5e-15; Mismatches 50; Indels 35; Gaps 9;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

Qy 20 VRLVVLVLTFLGAPCPAPL----PSCKEDBYPVGSECCPKCSPGVRKBEAGELTGTV 74
Db 1 MYRLPQCVING--CULTAVHPEPPFACREKOYLNSQCSLCPGQKLNSDCTEFTETE 58

Qy 75 CEPCPGTYYAHNLGSKCLOCOMCDPAMGLRASRNCSRTENAVCGSPGHFCIVQDGHD 134
Db 59 CLPGGSBBFLDTWNRATHCHOKYCDPNLGLRVQOKGTSETDITCICCEGHMC--TSEA 115

Qy 135 CAACRAYATSSPGQRVQKGGETSQDPTCQCCPCTYAHNLGSKCLOCOM 98
Db 116 CESCVLIGSCSPGFGVKQIATGVSPTCCEPCPVGFSSNVSAFEKCHPWTSCETKDLVQ 175

Qy 192 AGAGTSSSHWVWWFLSSLVIVCSTVGLICVRRKRPRGDVWKVIVSQRKRQEAE 251
Db 176 Q-AGTNKTDVWGPQLRRAWVPIFLGILFA-----ILLVVFIKKVAKKPTNK 225

Qy 252 ATVIEALQAPPDV-----TVAVEETI 273
Db 226 AP--HPKQEPQEBINFFDLFSNTAAFPVQETL 255

Search completed: November 14, 2003, 17:37:15
Job time : 31 secs

us-08-741-095b-26.rabp

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; SEQ ID NO: 18
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(38)
; US-09-934-289A-18

; RESULT 12
; Query Match 67.2%; Score 1060; DB 10; Length 197;
; Best Local Similarity 98.4%; Pred. No. 3.9e-82; Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
; Db 1 MEPPGDWGPWRSPRTDVLRLVLYLTFGAPCYAPALSKCDEDYPVSSECCPKCSFG 60
; Qy 1 YRVKEARCGELTGIVCPCPGTYIAHNGISKLCQCMCDPAMGLRASRNCSRTENAVCG 120
; Db 61 CSPGHRCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Qy 121 CSPGHRCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Db 121 CSPGHRCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Qy 181 HQTKCSW 187
; Db 181 HQT--NW 185

; RESULT 11
; Query Match 67.2%; Score 1060; DB 10; Length 197;
; Best Local Similarity 98.4%; Pred. No. 3.9e-82; Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
; Db 1 MEPPGDWGPWRSPRTDVLRLVLYLTFGAPCYAPALSKCDEDYPVSSECCPKCSFG 60
; Qy 1 YRVKEARCGELTGIVCPCPGTYIAHNGISKLCQCMCDPAMGLRASRNCSRTENAVCG 120
; Db 61 CSPGHRCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Qy 121 CSPGHRCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Db 121 CSPGHRCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Qy 181 HQTK 184
; Db 181 HQTK 184

; RESULT 12
; Sequence 4, Application US/09934289A
; Patent No. US20020132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERBESVIRUS-ENTRY-MEDIATOR-RELATED PROTEIN FAMILY AND USES THEREOF
; TITLE OF INVENTION: HERBESVIRUS-ENTRY-MEDIATOR-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB1098-061C1CN1(M)
; CURRENT APPLICATION NUMBER: US/09/934 , 289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ For Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-934-289A-4

; RESULT 13
; Query Match 53.7%; Score 847; DB 10; Length 155;
; Best Local Similarity 98.0%; Pred. No. 3.3e-64; Matches 146; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
; Db 1 LPSCKEDEPVGSSCCPKCSPGVRVKEACGELTGIVCPCPGTYIAHNGISKLCQCM 98
; Qy 1 99 CDPMGLRASRNCSRTENAVCGSPGPHCIVDGDHCAACRAVATSSPGQRVQKGGSQ 158
; Db 61 CDPAMGLRASRNCSRTENAVCGSPGPHCIVDGDHCAACRAVATSSPGQRVQKGGSQ 120
; Qy 159 DTLCONCPGTFSPNGTLEECOHOTKCSW 187
; Db 121 DTLCONCPGTFSPNGTLEECOHOTKCSW 149

; RESULT 13
; Sequence 32, Application US/09934289A
; Patent No. US20020132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERBESVIRUS-ENTRY-MEDIATOR-RELATED PROTEIN FAMILY AND USES THEREOF
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERBESVIRUS-ENTRY-MEDIATOR-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB1098-061C1CN1(M)
; CURRENT APPLICATION NUMBER: US/09/934 , 289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ For Windows Version 3.0
; SEQ ID NO: 32
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-934-289A-32

; RESULT 13
; Query Match 53.4%; Score 843; DB 10; Length 148;
; Best Local Similarity 100.0%; Pred. No. 6.9e-54; Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Db 1 YRVKEARCGELTGIVCPCPGTYIAHNGISKLCQCMCDPAMGLRASRNCSRTENAVCG 120
; Qy 121 CSPGHFCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Db 121 CSPGHFCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Qy 61 YRVKEARCGELTGIVCPCPGTYIAHNGISKLCQCMCDPAMGLRASRNCSRTENAVCG 120
; Db 61 YRVKEARCGELTGIVCPCPGTYIAHNGISKLCQCMCDPAMGLRASRNCSRTENAVCG 120
; Qy 121 CSPGHFCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180
; Db 121 CSPGHFCIVDGDHCAACRAVATSSPGQRVQKGGSQDTCQNCOPPGTSPNGTLEEQ 180

```

DE Tumor necrosis factor receptor II homolog.
 GN CRMb
 OS Camelpox virus (strain CP-1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 RN EMBL_TaxID-203174;
 [1] RPLSEQUENCE FROM N.A.
 RP STRAIN=DUBAI-1992 / CP-5, and SOMALIA-1978;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U87840; AAB94357_1; -.
 DR HSSP; Q92956; 1UMA.
 DR InterPro IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 SMART; SW00208; TNFR_c6; 2.
 PROSITE; PS00050; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 SQ SEQUENCE 349 AA; 38036 MW; EA412AEE86B090E4 CRC64;

Query Match 16.9%; Score 266.5; DB 12; Length 349;
 Best Local Similarity 33.1%; Pred. No. 2.1e-18;
 Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

QV 21 LRLVLYLTFLGAPC-----YAPALPSCKEDBYPGVSECCPKKPGYRKVEAGEL 70
 Db 1 MRSVLYSYIYLFLSCITINGRDIAPHA
 [1] PGSNGKCKDNERYRSRNLLCCLSCPPGTYASRLLCDSK 60

DR 71 TGTVCVERCPGTYIAHNGLSKLCQO-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
 AC 61 TNTQCTPCGSDFTSRNHLQACLSNGRCDD-SNOVETRSNTTHRNICCSPGYCLL 118

QV 71 TGTVCVERCPGTYIAHNGLSKLCQO-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 orthopoxviruses to a particular species.",
 DR Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U87843; AAB94360_1; -.
 DR HSSP; Q92956; 1UMA.
 DR InterPro; IPR001368; TNFR_c6; 2.
 DR Pfam; PF00020; TNFR_c6; 2.
 SMART; SW00208; TNFR_c6; 2.
 DR PROSITE; PS00050; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 DR Receptor.

RRESULT 14
 057103 PRELIMINARY; PRT; 348 AA.
 ID 057103:
 AC 057103:
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Tumor necrosis factor receptor II homolog.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 RN EMBL_TaxID-10244;
 [1] RPLSEQUENCE FROM N.A.
 RP STRAIN=Sierra Leone-1970;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 orthopoxviruses to a particular species.",
 DR Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U87843; AAB94360_1; -.
 DR HSSP; Q92956; 1UMA.
 DR InterPro; IPR001368; TNFR_c6; 2.
 DR Pfam; PF00020; TNFR_c6; 2.
 SMART; SW00208; TNFR_c6; 2.
 DR PROSITE; PS00050; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 DR Receptor.

SQ SEQUENCE 349 AA; 38321 MW; FE449028CC933F57 CRC64;

Query Match 16.8%; Score 265.5; DB 12; Length 349;
 Best Local Similarity 32.6%; Pred. No. 2.6e-18;
 Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QV 21 LRLVLYLTFLGAPC-----YAPALPSCKEDBYPGVSECCPKKPGYRKVEAGEL 70
 DR 1 MRSVLYSYIYLFLSCITINGRDIAPHA
 [1] PGSNGKCKDNERYRSRNLLCCLSCPPGTYASRLLCDSK 60

QV 71 TGTVCVERCPGTYIAHNGLSKLCQO-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
 DR 61 TNTQCTPCGSDFTSRNHLQACLSNGRCDD-SNOVETRSNTTHRNICCSPGYCLL 118

QV 130 QGDHCAACRAYATSSFGQRVKGGTESQDTLQCONCPGTFSPN-GTLECOHOT 183
 DR 119 KGALGERTCISLKCGIGYGV-SGYTSTGDVIVCSPCCPGTYSHTVSSDKCPEPV 172

QV 190 T 190
 DR 173 T 173

Query Match 16.8%; Score 265.5; DB 12; Length 348;
 Best Local Similarity 32.0%; Pred. No. 2.6e-18;
 Matches 56; Conservative 25; Mismatches 79; Indels 15; Gaps 5;

QV 21 LRLVLYLTFLGAPC-----YAPALPSCKEDEVPGVSECCPKKPGYRKVEAGEL 70

Search completed: November 14, 2003, 17:31:45
 Job time : 43 secs

KW	Receptor.
SQ	SEQUENCE 348 AA; 38212 MW; E555979057DBC91F CRC64;
Query	Match 17.1%; Score 269.5; DB 12; Length 348; Best Local Similarity 32.6%; Pred. No. 1e-18; Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;
Db	21 LRLVLYLTFLGAPC-----YAPALPSCKEDEPVGSECCPKCSPGYRKACCEL 70 1 MRSVLYSYILFLSCLTINGRDIAPHAPSNGKCKDNBYRSRNLLCSCPPGTYSYLRLCDSK 60
Qy	71 TGTVCERCPGTYIAHNGLSKLCQO-MCDPAMGLRASNRNCSRTENAVCGCSPGHFCIV 129 61 TNTQCTPCGSDFTSHNNHLQACLSNCGRCD--SNOVETRSNTTHNRICCESPGYCULL 118
Db	130 QDGDHCAACRAYATSSPGQAVQKGGETESQPTLCONCOPPGTFSPN-GTLEBCQHQT 183 119 KGSSGRCITCISKTKGIGYGV-SGYTSTGDIVCSPCGPGTYSHTVSSTDKCEPV 172
Qy	71 TGTVCERCPGTYIAHNGLSKLCQO-MCDPAMGLRASNRNCSRTENAVCGCSPGHFCIV 129 61 TNTQCTPCGSDFTSHNNHLQACLSNCGRCD--SNOVETRSNTTHNRICCESPGYCULL 118
Db	130 QDGDHCAACRAYATSSPGQAVQKGGETESQPTLCONCOPPGTFSPN-GTLEBCQHQT 183 119 KGSSGRCITCISKTKGIGYGV-SGYTSTGDIVCSPCGPGTYSHTVSSTDKCEPV 172
RESULT 8	
O57277	PRELIMINARY; PRT; 348 AA.
ID	O57277; AC
DT	01-JUN-1998 (TREMBLrel. 06, Created) 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Tumor necrosis factor receptor II homolog (J2L).
GN	CRMB OR J2R OR J2L.
OS	Monkeypox virus
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC	Orthopoxvirus.
OX	Orthopoxvirus.
RN	[1] SEQUENCE FROM N.A.
RP	STRAIN=Zaire-1977;
RC	Loparev V.N., Parsons J.M., Esposito J.J.; Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases. [2]
RA	Loparev V.N., Parsons J.M., Esposito J.J.; Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=Zaire-96-I-16;
RX	MEDLINE:21592287; PubMed:11734207;
RA	Shchelkunov S.N., Notmeier A.V., Babkin I.V., Safronov P.F., Ryzankina O.I., Petrov N.A., Guturov V.V., Uvarova E.A., Mikhnev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B., Sandakchiev L.S.; "Human monkeypox and smallpox viruses: genomic comparison."; FEBS Lett. 503:66-70(2001).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Zaire-96-I-16;
RA	Shchelkunov S.N., Totmenin A.V., Safronov P.F., Guturov V.V., Ryzankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A., Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakchiev L.S.; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL	EMBL; U89453; AAB94378.1; -. EMBL; U87841; AAB94358.1; -. EMBL; AF080133; AAI40648.1; -. EMBL; AF080138; AAI40460.1; -.
DR	HSSP; Q22956; 1JMA.
DR	InterPro; IPR01368; TNFR_C6.
DR	Pfam; PF00020; TNFR_C6; 2.
DR	SMART; SM00028; TNFR; 2.
DR	PROSITE; PS00052; TNFR_NGFR_2; 2.
DR	PFAM; PF00020; TNFR_C6; 2.
DR	SMART; SM00028; TNFR; 2.
DR	SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;
Query	Match 17.1%; Score 269.5; DB 12; Length 348; Best Local Similarity 32.6%; Pred. No. 1e-18; Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5; Gaps 5;
Db	21 LRLVLYLTFLGAPC-----YAPALPSCKEDEPVGSECCPKCSPGYRKACCEL 70 1 MRSVLYSYILFLSCLTINGRDIAPHAPSNGKCKDNBYRSRNLLCSCPPGTYSYLRLCDSK 60
Qy	71 TGTVCERCPGTYIAHNGLSKLCQO-MCDPAMGLRASNRNCSRTENAVCGCSPGHFCIV 129 61 TNTQCTPCGSDFTSHNNHLQACLSNCGRCD--SNOVETRSNTTHNRICCESPGYCULL 118
Db	130 QDGDHCAACRAYATSSPGQAVQKGGETESQPTLCONCOPPGTFSPN-GTLEBCQHQT 183 119 KGSSGRCITCISKTKGIGYGV-SGYTSTGDIVCSPCGPGTYSHTVSSTDKCEPV 172
RESULT 9	
O57101	PRELIMINARY; PRT; 349 AA.
ID	O57101; AC
DT	01-JUN-1998 (TREMBLrel. 06, Created) 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Tumor necrosis factor receptor II homolog.
GN	CRMB.
OS	Monkeypox virus
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC	Orthopoxvirus.
OX	Orthopoxvirus.
RN	[1] SEQUENCE FROM N.A.
RP	STRAIN=Zaire-1977;
DR	Loparev V.N., Parsons J.M., Esposito J.J.; Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR	EMBL; U87845; AAB94362.1; -.
DR	HSSP; Q9256; 1JMA.
DR	InterPro; IPR001368; TNFR_C6.
DR	PFam; PF00020; TNFR_C6; 2.
DR	SMART; SM00028; TNFR; 2.
DR	PROSITE; PS00052; TNFR_NGFR_1; 2.
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.
DR	SEQUENCE 349 AA; 38311 MW; 02F65B00CFB858BE CRC64;
Query	Match 17.1%; Score 269.5; DB 12; Length 349; Best Local Similarity 32.6%; Pred. No. 1e-18; Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5; Gaps 5;
Db	21 LRLVLYLTFLGAPC-----YAPALPSCKEDEPVGSECCPKCSPGYRKACCEL 70 1 MRSVLYSYILFLSCLTINGRDIAPHAPSNGKCKDNBYRSRNLLCSCPPGTYSYLRLCDSK 60
Qy	71 TGTVCERCPGTYIAHNGLSKLCQO-MCDPAMGLRASNRNCSRTENAVCGCSPGHFCIV 129 61 TNTQCTPCGSDFTSHNNHLQACLSNCGRCD--SNOVETRSNTTHNRICCESPGYCULL 118
Db	130 QDGDHCAACRAYATSSPGQAVQKGGETESQPTLCONCOPPGTFSPN-GTLEBCQHQT 183 119 KGSSGRCITCISKTKGIGYGV-SGYTSTGDIVCSPCGPGTYSHTVSSTDKCEPV 172
Qy	190 T 190
Db	173 T 173
RESULT 10	
O57102	PRELIMINARY; PRT; 349 AA.
ID	O57102; AC
DT	01-JUN-1998 (TREMBLrel. 06, Created) 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Tumor necrosis factor receptor II homolog.
GN	CRMB.
OS	Monkeypox virus
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

YATSSPQQRVQKGCTESQDTLCONCPGFTS-PNGTLECOHQTKC-SWLVTKAGAGTSS 198
 ::|||::|||::|||::|||::|||::|||::|||:
 122 HSLCFPGIGVKOMATEVSDTICEPCPVGFSENVSASEKQWPWSSESKQGIVEQFRAGTNK 181
 GN CRMB.

SHWWWWFLSGSLIVIVTCSTVGLLICVKKRKRERGRGDVVKVTVSQVRKRQEAESEA----- 252
 ::|||::|||::|||::|||:
 182 TDVVCFFQSRMRLALVVIPIITGILPA-----VLLVFLCIRKVTKEOBTKALHPTE 232
 OS Monkeypox virus.

SHWWWWFLSGSLIVIVTCSTVGLLICVKKRKRERGRGDVVKVTVSQVRKRQEAESEA----- 252
 ::|||::|||::|||:
 253 --TVIKA--LQARPPDVYTVAVEETI 273
 OC DNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

Db RDPVERHIDLEFPD-STAPVQETL 256
 OC Orthopoxvirus
 OC NCBITaxID=10244;
 RC SEQUENCE FROM N.A.
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT STRAIN=Nigeria-1971;
 RT "DNA sequence analysis as a criterion for allocation of the
 orthopoxviruses to a particular species.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Q92956; JMA;
 DR HSSP; Q92956; JMA;
 DR Inter-Pro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 KW RECEPTOR.
 SQ SEQUENCE. 349 AA; 38239 MW; DF6C280D478F2422 CRC64;
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029254; AAC029254 1; "Myb-DNA binding."
 DR Inter-Pro; IPR001005; Myb-DNA binding.
 DR Inter-Pro; IPR001865; Ribosomal_S2.
 DR Inter-Pro; IPR001368; TNFR_c6.
 DR Pfam; PF0002; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00037; TNFR_1; 1.
 DR PROSITE; PS0062; RIBOSOMAL_S2_1; 1.
 DR PROSITE; PS0052; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 KW Receptor.
 SQ SEQUENCE. 289 AA; 32077 MW; DBE93B13439F1E2A CRC64;
 Query Match 17.8%; Score 280 5; DB 11; Length 289;
 Best Local Similarity 27.9%; Pred. No. 6.6e-20; Indels 29; Gaps 8;
 Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;
 Gaps 5;
 QY 41 SCKEDBYPVSEBCCIKCSPQSYRKVKEACGETTGTVCEPCPPGTAYHLNGISKCLQCQMCQ 100
 ::|||::|||::|||::|||::|||::|||:
 25 TCSDKOYLHQQCCDLCQPSRLTSHTCALEKTOCHPCDSGEFSAQWNREBIRCHORHCE 84
 AC 057108 PRELIMINARY; PRT; 348 AA.
 Db 101 PAMGLRASRCSRRTENAVCCGSPGFCIVGDDHCAACRAYATSSPGQWQKGCTESQDTLCONCPGFTS-N 160
 ::|||::|||::|||::|||::|||:
 85 PNQGLRKVKKGTAESDPTVCKEGEGHCTSD--CEACQHTPCIPGFGNEMATTUT 141
 AC 057108 PRELIMINARY; PRT; 348 AA.
 Db 161 LCQNCPPGTTSPNGTIEECQHQTCKS---WLVTKAGACTSSSHWWWWFLSGSLIVIV 215
 ::|||::|||::|||::|||:
 142 VCHPEPVGFISNSQSLFEKQYPWTSCEDKNEVQK---GTSQDNVICGKSKRMHALLVI 198
 AC 057108 PRELIMINARY; PRT; 348 AA.
 Db 216 CSTVGILITC-----VKR--RKPRGDVVKVIVSVORKRQAEGATVIAQAPPDVMT 266
 ::|||::|||::|||:
 199 PVMGILITFGVFLYIKKVVKPKDN--DILPPARRQDPOQEME-----DYPGHNTA 249
 AC 057100 PRELIMINARY; PRT; 349 AA.
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

RESULT 5
 PRELIMINARY; PRT; 289 AA.
 ID Q8K2X6
 AC Q8K2X6;
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Similar to tumor necrosis factor receptor superfamily, member 5.
 OS Mus musculus (Mouse);
 OC Buxkayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBITaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029254; AAC029254 1; "Myb-DNA binding."
 DR Inter-Pro; IPR001005; Myb-DNA binding.
 DR Inter-Pro; IPR001865; Ribosomal_S2.
 DR Inter-Pro; IPR001368; TNFR_c6.
 DR Pfam; PF0002; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00037; TNFR_1; 1.
 DR PROSITE; PS0062; RIBOSOMAL_S2_1; 1.
 DR PROSITE; PS0052; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 KW Receptor.
 SQ SEQUENCE. 349 AA; 38239 MW; DF6C280D478F2422 CRC64;
 Query Match 17.2%; Score 271.5; DB 12; Length 349;
 Best Local Similarity 32.6%; Pred. No. 6.6e-19; Indels 59; Gaps 5; Mismatches 59; Conservative 23; Gaps 19; Gaps 5;
 Gaps 5;
 QY 21 LRLVLYLTIGARC-----YAPALPSCKEDEYVPGSECCKPKSGPYRVEKAQEL 70
 ::|||::|||::|||::|||:
 1 MRSVLYSYVLFLSCLININGRDIAFHAPSNGKCKDNERYRSRNLLCCLSCPPGTYASRLCDSK 60
 AC 057108 PRELIMINARY; PRT; 348 AA.
 Db 71 TGTWCBCPGPTVIAHNLNGISKLQOCQ-MCDPAMGLRASRNCRTERNAVCGSPGPHCIV 129
 ::|||::|||::|||:
 61 TINTQPCCSDTFPCSDTNPQHNLQATLSCNRCR--SNQVTRSCNTHRICESSPGYCIL 118
 AC 057108 PRELIMINARY; PRT; 348 AA.
 Db 130 QDGDHCAAGRAYATSSPGQVQKGCTESQDTLCONCPGFTS-N 169
 ::|||::|||:
 119 KGAGSCSICISKVKOGIGIGV-SGVTSTGVDICSPCGFTS---HTVSSIDKCPWV 172
 AC 057108 PRELIMINARY; PRT; 348 AA.
 Db 190 T 190
 QY 190 T 190
 AC 057108 PRELIMINARY; PRT; 348 AA.
 Db 173 T 173
 QY 173 T 173
 RESULT 7
 PRELIMINARY; PRT; 348 AA.
 ID 057108
 AC 057108; PRELIMINARY; PRT; 348 AA.
 Db 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Tumor necrosis factor receptor II homolog.
 GN CRMB.
 OS Monkeypox virus.
 OC DNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Faure-1970;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 orthopoxviruses to a particular species.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EML; U88142; AAC94367.1; -.
 DR HSSP; Q92956; JMA.
 DR Inter-Pro; IPR001368; TNFR_c6.
 DR Pfam; PF0002; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS0062; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.

RESULT 6
 PRELIMINARY; PRT; 349 AA.
 ID 057100
 AC 057100;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)

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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:28:10 ; Search time 41 Seconds

1781.192 Million cell updates/sec

Title: US-08-741-095B-26
Perfect score: 1578
Sequence: 1 MEPPGDWGPWMSITPRTDV..... VTTVAVETIPSFTGSPN 283

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 25802604 residues

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0

Maximum DB seq length: 280000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL_23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_micr:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriaph:
17: sp_archeap:
Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1303.5	82.6	283	6 Q9XSZB
2	62.0	283	6 Q9XSZB	O9xsz8 cercopithec
3	384.5	199	4 Q8N634	Q8n634 homo sapien
4	24.4	196	11 Q8VC17	Q8vc17 mus musculu
5	332	21.0	6 Q8S034	Q8s034 sus scrofa
6	280.5	17.8	6 Q8K2X6	Q8k2x6 mus musculu
7	271.5	17.2	11 Q5T100	Q5t100 monkeypox v
8	269.5	17.1	12 Q5T108	Q5t108 monkeypox v
9	269.5	17.1	12 Q5T277	Q5t277 monkeypox v
10	269.5	17.1	12 Q5T101	Q5t101 monkeypox v
11	269.5	17.1	12 Q5T102	Q5t102 monkeypox v
12	266.5	16.9	12 Q5T291	Q5t291 monkeypox v
13	266.5	16.9	12 Q5T098	Q5t098 camelpox vi
14	265.5	16.8	12 Q5T284	Q5t284 camelpox vi
15	265.5	16.8	12 Q5T103	Q5t103 monkeypox v
16	262.5	16.6	12 Q5T099	Q5t099 monkeypox v
17	262	16.6	11 Q9JHE0	Q9jhe0 ratus norv
18	259	16.4	12 Q5T111	Q5t111 variola vir
19	257.5	16.3	12 Q5T112	Q5t112 variola vir
20	257.5	16.3	12 Q5T117	Q5t117 cowpox viru
21	257	16.3	6 Q8WMQ2	Q8wmq2 ovis aries
22	257	16.3	12 Q5T110	Q5t110 variola vir
23	254.5	16.1	12 Q9DfV0	Q9dfv0 brachydanio
24	249	15.8	12 Q5T109	Q5t109 variola vir
25	239	15.1	12 Q5T116	Q5t116 cowpox viru
26	236.5	15.0	12 Q5T121	Q5t121 cowpox viru
27	232.5	14.7	12 Q5T122	Q5t122 cowpox viru
28	229.5	14.5	12 Q5T119	Q5t119 cowpox viru
29	229	14.5	12 Q5T120	Q5t120 cowpox viru
30	228	14.5	12 Q5DGR8	Q5dgr8 gallus gallu
31	228	14.4	12 Q8G9H8	Q8g9h8 gallus gallu
32	228	14.4	12 Q5T118	Q5t118 cowpox viru
33	227	14.4	12 Q9DGH7	Q9dgh7 gallus gallu
34	226.5	14.4	12 Q5T123	Q5t123 cowpox viru
35	225.5	14.3	12 Q5T115	Q5t115 cowpox viru
36	225.5	14.3	12 Q85308	Q85308 cowpox viru
37	219.5	13.9	6 Q9T764	Q9t764 oryctolagus
38	219.5	13.9	6 Q9TV79	Q9tv79 oryctolagus
39	218	13.8	6 Q9KS29	Q9ks29 oryctolagus
40	218	13.8	11 Q91ZM6	Q91zm6 ratituss norv
41	216	13.7	6 Q9BDP0	Q9bdp0 aotus trivi
42	215.5	13.7	6 Q9XS60	Q9xs60 oryctolagus
43	214.5	13.6	4 Q8IV86	Q8iv86 homo sapien
44	213.5	13.5	320 12 Q5T079	Q5t079 cowpox viru
45	213.5	13.5	417 11 Q8ByY1	Q8byy1 mus musculu

ALIGNMENTS

RESULT 1

ID Q9XSZB PRELIMINARY; PRT; 283 AA.
AC Q9XSZB;
DT 01-NOV-1999 (TREMBREL. 12, Created)
DT 01-MAR-2003 (TREMBREL. 23, Last sequence update)

DE Hvea.

GN [1] — HYDAS.

OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.

NCBI_TaxID=9334; RT Hvea.

SEQUENCE FROM N.A.
RC TISSUE=Kidney;

RX MEDLINE=99296730; PubMed=10366573;

RA Foster T.P., Chouljenko V.N., Kousoulas K.G.; "Functional characterization of the Hvea homolog specified by African

green kidney kidney protein with a herpes simplex virus expressing the green fluorescence protein."

RT Vitrology 258:365-74(1999).

RL EMBL; AF147720; AAD37381.1; -.

DR HSSP; Q92956; 1JMA;

DR InterPro; IPR001168; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 3.

DR SMART; SMC008; TNFR;

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS05050; TNFR_NGFR_2; 2.

SQ SEQUENCE 283 AA; 30199 NM; 397951C6617FE3AA CRC64;

Query Match 82.6%; Score 1303.5; DB 6; Length 283;

Best Local Similarity 82.0%; Pred. No. 1.2e-122; Matches 232; Conservative 18; Mismatches 30; Indels 3; Gaps 2;

QY 1 MEPPGDWGPWMSITPRTDVLRVLYLTPFLGARYALPSCKEDEPVGSECCPKSPG 60

Db 1 MEPPGGWGSPPRRPAPKADILTVLYUTPLGSSCYAPALPSCKEDEVPGSECCPKSPG 60

QY 1 MEPPGGWGSPPRRPAPKADILTVLYUTPLGSSCYAPALPSCKEDEVPGSECCPKSPG 60

Db 1 MEPPGGWGSPPRRPAPKADILTVLYUTPLGSSCYAPALPSCKEDEVPGSECCPKSPG 60

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Search completed: November 14, 2003, 17:30:50
 Job time : 18 secs

CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
 CC both (By similarity).
 CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSMIC ADAPTER PROTEINS.
 CC -!- SIMILARITY: Contains 3 TNFR-CYS repeats.
 CC -!- SIMILARITY: Contains 1 death domain.

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CC or send an email to license@isb-sib.ch.

CC

DR EMBL; AJ001202; CA04596.1; - .

DR HSSP; P2145; 1DDF.

DR InterPro; IPR00048; Death.

DR InterPro; IPR001368; TNFR_C6.

DR pfam; PF00531; death; 1.

DR pfam; PF00020; TNFR_C6; 3.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR_NGFR; 1; 2.

DR PROSITE; PS50050; TNFR_NGFR; 2; 2.

DR PROSITE; PS50017; DEATH DOMAIN; 1.

KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 332 POTENTIAL.

FT DOMAIN 17 175 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 6.

FT TRANSMEM 176 192 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 193 332 POTENTIAL.

FT REPEAT 45 81 CYTOPLASMIC (POTENTIAL).

FT REPEAT 82 125 TNFR-CYS 1.

FT REPEAT 126 164 TNFR-CYS 3.

FT DOMAIN 227 311 DEATH.

FT DISULFID 46 57 BY SIMILARITY.

FT DISULFID 58 71 BY SIMILARITY.

FT DISULFID 61 80 BY SIMILARITY.

FT DISULFID 83 99 BY SIMILARITY.

FT DISULFID 102 117 BY SIMILARITY.

FT DISULFID 105 125 BY SIMILARITY.

FT DISULFID 127 141 BY SIMILARITY.

FT DISULFID 144 155 BY SIMILARITY.

FT DISULFID 147 163 BY SIMILARITY.

FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 332 AA; 37592 MW; 580B03682756BF1B CRC64;

Query Match 15.0%; Score 236; DB 1; Length 332;
 Best Local Similarity 27.5%; Pred. No. 7.9e-12; Gaps 9;
 Matches 65; Conservative 30; Mismatches 95; Indels 46;

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QY 42 CKEDEPVPGSBCCPKCSPGVKEACGELGTG-VCEPCPPG-TWIAHNGLISKCQOCMC 99
Db 46 CPEGQHREGQQFCQCQCPGPGRKHADCTSPGAGAPCVCPCSEGEDYTDKNHHSKCCRRCRV 105
  100 DPAMGLRASRNSRSRERENAVGCGSCCHFCITVQDGHCACRABAYTSSHHWWFLGSLSVIVIGS 159
  106 DGEHGLEVEKNCTQTKCRCKPNPFCHTSQCEHNPCT----- 144
  160 TLQNCQPPGTFSPNGLTGC-QHQTKCSWLVTKAGAGTSSSHAWWWFLGSLSVIVIGS 217
  145 TTCB-----HGVIENTPTSMTKCREFQSGS-RSNLHNW---ALLLIPVA 190
  218 TVGLLTCVKRKPRGDVVKVIVSVORKRQEAEGETVIALQAPPDVTVAVEETI 273
  191 LVRKVVKRCKRKENGQKITS----NAE-EVPMIKUDLGKYITRAEQMKI 239

```


Matches 69; Conservative 16; Mismatches 88; Indels 22; Gaps 8;

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CC

QY 16 PRTDVLRLVILFLIGACPVAPALPSCKE-DEXP----VGSR-CCPKCSPYRVEKACG 68

CC

Db 7 PSHSILCLVLALPAL--LPPAVRGVAETPTPFWRDAETGERLIVCAQCPGTFVOPCR 63

DR EMBL; U29173; AAA68964.1; --

DR EMBL; U38423; AAB0846.1; --

DR HSSP; 014763; IDOG.

DR MGI; MGI:04875; Ltbr.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF0002; TNFR_c6; 3.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR_NGR; 1; 2.

DR PROSITE; PS50050; TNFR_NGR_2; 3.

KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 30

FT CHAIN 31 415

FT DOMAIN 31 223

FT TRANSMEM 224 244

FT DOMAIN 245 415

FT REPEAT 42 81

FT REPEAT 82 124

FT REPEAT 125 170

FT REPEAT 171 213

FT DISULFID 43 58

FT DISULFID 59 72

FT DISULFID 62 80

FT DISULFID 83 98

FT DISULFID 101 116

FT DISULFID 104 124

FT DISULFID 126 132

FT DISULFID 139 150

FT DISULFID 142 169

FT DISULFID 172 187

FT CARBOND 40 40

FT CARBOND 179 179

SQ SEQUENCE FROM N.A. 415 AA; 44956 MW; 29B32A56AEFF61 CRC64;

RX MEDLINE=9602804; PubMed=7594541;

RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,

RA Browning J.L., Ware C.F.;

RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding, and expression."; RT Immunol. 155:5280-5288(1995).

[2] SEQUENCE FROM N.A.

RX MEDLINE=96163885; PubMed=8586432;

RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,

RA Honjo T.; RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping."; RT Genomics 30:312-319(1995).

RN [3]

RN INTERACTION WITH TRAF5.

RX STRAIN=BALB/C;

RA MEDLINE=96278943; PubMed=8663299;

RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,

RA Yagita H., Okumura K.;

RT TRAF5, an activator of NF-kappaB and putative signal transducer for the lymphotoxin-beta receptor. J. Biol. Chem. 271:14661-14664(1996).

CC -!- BIOL: Receptor for the heterotrimeric lymphotoxin containing LTA and LTb, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs (BY similarity). SUBUNIT: Self-associates (BY similarity); Associates with TRAF5. Associates with TRAF3 and TRAF4 (BY similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

RESULT 12

CC CRMB_COWPX STANDARD; PRT; 351 AA.

CC

Db ID CRMB_COWPX

Db AC 073559; 28-FEB-2003 (Rel. 41, Created)

Db DT 28-FEB-2003 (Rel. 41, Last sequence update)

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QY	117	TSKRKTQRCOPGMCAAW-ALECHCBLISDCPGEATEBLKDEVKGKNNH-----CVPC	RA	Raha S.S., loqueillano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
166	PPGTPF----SPNGTILEECQHQTKC-SWLVTKAGRTQSSHHWWV-----FLGSLVT	212	RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
	: : ; : : : : : : : : : : : : : : : :		RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huyk S.W.,
171	KAGHFOQTSSPA--RCQHTRCENQGLVEAAGCTAQSDTCNPLELPPMNSGTM	227	RA	Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A.,
	: : : : : : : : : : : : : : : : : : :		RA	Fahey J., Heiton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
			RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
			RA	Blakesley R.W., Touchman J.W., Grimwood J., Schmutz J., Myers R.M.,
			RA	Rodriguez A.C., Butterfield Y.S.N., Kitzwinski M.I., Skalaska U., Snailius D.E.,
			RA	Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.,
			RA	"Generation and initial analysis of more than 15,000 full-length
Db	228 LAVILPLAFLILLATVFSCIWKSHP--SLCRKLGSLLKRRPQGEGPNPVAGSWPPKAMP	285	RT	human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
QY	262 --PDVTVAVEETPSFTGRSP 281		RL	-!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT
Db	286 YFPDID--VQPLPIPISGGDVP 303		CC	and TNFSF6/FASL. Protects against apoptosis.
RESULT 10			CC	-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
TR6B_HUMAN	STANDARD:	PRT: 300 AA.	CC	CC
ID: TR6B_HUMAN			CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
AC: O93407;			CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
DT: 28-FEB-2003 (Rel. 41, Created)			CC	the European Bioinformatics Institute. There are no restrictions on its
DT: 15-SEP-2003 (Rel. 42, Last annotation update)			CC	use by non-profit institutions as long as its content is in no way
DE: Tumor necrosis factor receptor superfamily member 6B precursor (Decoy			CC	modified and this statement is not removed. Usage by and for commercial
receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).			CC	entities requires a license agreement (see http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
GN: TNFRSF6B OR DCR3 OR TR6.			CC	
OS: Homo sapiens (Human).			CC	CC
OC: Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			CC	CC
OC: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			CC	CC
OX: NCBI_TaxID=9606;			CC	CC
RN: [1]			CC	CC
RP: SEQUENCE FROM N.A.			CC	CC
RC: TISSUE:Fetal lung;			CC	CC
RX: MEDLINE-99087326; PubMed=9872321;			CC	CC
RA: PITT1 R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,			CC	CC
RA: Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,			CC	CC
RA: Godowski P.J., Wood M.J., Gurney A.L., Hillan K.J., Cohen R.L.,			CC	CC
RA: Godowski A.D., Bottstein D., Ashkenazi A.;			CC	CC
RT: "genomic amplification of a decoy receptor for Fas ligand in lung and			CC	CC
RT: colon cancer"; Nature 396:699-703(1998).			CC	CC
RN: [2]			CC	CC
RP: SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.			CC	CC
RC: TISSUE:Prostate;			CC	CC
RX: MEDLINE-99253915; PubMed=10318773;			CC	CC
RA: Yu K.-Y., Kwon B.-J., Jin J., Zhai Y., Ebner R., Kwon B.-S.;			CC	CC
RT: "A newly identified member of tumor necrosis factor receptor			CC	CC
RT: superfamily (TR6) suppresses LIGHT-mediated apoptosis.,"			CC	CC
RL: J. Biol. Chem. 274:13733-13736(1999).			CC	CC
RN: [3]			CC	CC
RP: SEQUENCE FROM N.A.			CC	CC
RC: TISSUE:Lung;			CC	CC
RX: MEDLINE-20122600; PubMed=10655513;			CC	CC
RA: Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,			CC	CC
RA: Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;			CC	CC
RT: "Overexpression of gene amplification and its location in a four-gene			CC	CC
RT: independent of gene amplification and its location in a four-gene			CC	CC
RT: cluster."; Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).			CC	CC
RN: [4]			CC	CC
RP: SEQUENCE FROM N.A.			CC	CC
RA: Matthews L.;			CC	CC
RL: Submitted (Nov-2000) to the EMBL/GenBank/DBJ databases.			CC	CC
RN: [5]			CC	CC
RP: SEQUENCE FROM N.A.			CC	CC
RC: TISSUE:Lung, and Skin;			CC	CC
RX: MEDLINE-2238257; PubMed=1247932;			CC	CC
RA: Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			CC	CC
RA: Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			CC	CC
RA: Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			CC	CC
RA: Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			CC	CC
RA: Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			CC	CC
RA: Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C.,			CC	CC
RA: Best Local Similarity 15.6%; Score 246; DB 1; Length 300;			CC	CC
RA: N-LINKED (GLCNAC, . . .) (POTENTIAL).			CC	CC
RA: SBQUENCE 300 AA; 32679 MW; F90ABE33718449AF CRC64;			CC	CC

- OX NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=93252381; PubMed=8486360;
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
 RT "Construction and evaluation of a cDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.";
 RL Genomics 16:214-218(1993).
 RN [2] SUBSEQUENCE FROM N.A.
 RP TISSUE=lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Tohjikuni S., Carninci P., Prange C.,
 RA Rahm S.S., Loqueline N.A., Peters G.J., Abramson R.D., Mulhahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon K.J., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettemann M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouttard G.G.,
 RA Blakesley R.W., Touichman J.W., Green E., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E.,
 RA Schnerring A., Schein J.E., Jones J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3] FUNCTION.
 RP FUNCTION.
 RX MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
 RA Enrrebent B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.,
 RT "A lymphotxin-alpha-specific receptor.";
 RL Science 264:707-710(1994).
 RN [4] CHARACTERIZATION.
 RP FUNCTION.
 RX MEDLINE=9223511; PubMed=10207006;
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.,
 RA "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 death in HeLa cells.";
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 LIGHT-mediated apoptosis of tumor cells.";
 RT J. Biol. Chem. 274:11868-11873(1999).
 RN [5] FUNCTION.
 RP FUNCTION.
 RX MEDLINE=20261554; PubMed=10799510;
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 LIGHT-mediated apoptosis of tumor cells.";
 RT J. Biol. Chem. 275:14307-14315(2000).
 RN [6] INTERACTION WITH TRAF3.
 RP MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA "Yagita H., Okumura K.;
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
 the lymphotoxin-beta receptor";
 RT J. Biol. Chem. 271:14661-14664(1996).
 RN [7] INTERACTION WITH TRAF4.
 RP MEDLINE=9626059;
 RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
 RA Gascoyne R.D., Boreen K., McCadden D., Shabalaik A., Hugh J.,
 RA Reynolds C.V., Cleverley J.C., Reed J.C.,
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
 adult, fetal, and tumor tissues.";
 RT Am. J. Pathol. 152:1549-1561(1998).
 RN [8] TISSUE-lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klaunzer R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Tohjikuni S., Carninci P., Prange C.,
 RA Rahm S.S., Loqueline N.A., Peters G.J., Abramson R.D., Mulhahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon K.J., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettemann M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouttard G.G.,
 RA Blakesley R.W., Touichman J.W., Green E., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E.,
 RA Schnerring A., Schein J.E., Jones J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3] FUNCTION.
 RP INTERACTION WITH TRAF5.
 RX MEDLINE=98172745; PubMed=9511754;
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
 RA Otsuka M., Yamamoto T., Inoue J.-I.,
 RT "Cloning and characterization of a cDNA encoding the human homolog of
 tumor necrosis factor-associated factor 5 (TRAF5).";
 RT Gene 207:135-140(1998).
 CC FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs.
 CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
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 CC
 DR EMBL: L04270; AA36757.1; -.
 DR EMBL: BC06262; AAH6262.1; -.
 DR PIR: 154182; 151182.
 DR HSSP: P25942; LCDP.
 DR PROSITE: PS00652; LTPR.
 DR MIM: 600979; .
 DR GO: 6007165; P:signal transduction; TAS.
 DR InterPro: IPR003368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 KW SIGNAL; 1; 30
 FT CHAIN; 31; 435
 FT DOMAIN; 31; 227
 FT TRANSEM; 228; 248
 FT DOMAIN; 249; 435
 FT REPEAT; 42; 81
 FT REPEAT; 82; 124
 FT REPEAT; 125; 168
 FT REPEAT; 169; 211
 FT DISULFID; 43; 58
 FT DISULFID; 59; 72
 FT DISULFID; 62; 80
 FT DISULFID; 83; 98
 FT DISULFID; 101; 116
 FT DISULFID; 104; 124
 FT DISULFID; 126; 132
 FT DISULFID; 139; 148
 FT DISULFID; 142; 167
 FT DISULFID; 170; 185
 FT DISULFID; 40; 40
 FT CARBOHYD; 177; 177
 FT SEQUENCE; 435 AA; 46709 MW; 62462E602F56F crcc64;
 QY Query Match
 QY Best Local Similarity 26.7%; Score 253; DB 1; length 435;
 QY Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16;
 QY 4 PG-DWGGPPWMSTPRITDVLRLVLYTFL-----GAPCYAPALPCK--EDEY--PVGS 51
 Db 52 ECPKCGPGYRKEACCLTGIVCECPGTYIAHNGLSKQCOMCDPAMGLRASNC 111
 Db 57 ICCSRCPGTVYSAKCSRIRDPTVCATGAENSYNNHMYLTICQLCRCPDPVNGLEIAPC 116
 QY 10 PLGAWGP-----LVLGLGILAAASOPQAVPPYASENOQRDQEKEYESQH 56
 QY 112 SRTENAVPGCSPGHFCIVQDGHCACAGRAYATSSPG-----QRVQKGTSQDTLQNC 165

DE	Soluble TNF receptor II precursor (cytokine response modifying protein B).	DR	PIR; D72175; D72175.
CRMB OR G2R OR G4R.		DR	PIR; D72623; D72623.
Variola virus.		DR	HSSP; O14763; 1DQG.
OC viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;		DR	InterPro; IPR01348; TNFR_c6.
Orthopoxvirus;		DR	PFAM; PF00020; TNFR_c6_2.
NCBI_TaxID=10255;		DR	SMART; S00028; TNFR_c6_3.
RN [1]	SEQUENCE FROM N.A.	DR	PROSITE; PS00652; TNFR_NGFR_1; 2.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS55050; TNFR_NGFR_2; 2.
RC STRAIN=India-1967 / Isolate Ind3;		KW	Receptor; Glycoprotein; Repeat; Signal.
RX MEDLINE=9320281; PubMed=83881129;		FT	SIGNAL 1
RA Shchelkunov S.N.; Blinov V.M.; Sandakhchiev L.S.;		FT	SOLUBLE TNF RECEPTOR II.
RT "Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms".		FT	TNFR-CYS 1.
RT FEBS Lett. 319:80-83(1993).		FT	TNFR-CYS 2.
RN [2]	SEQUENCE FROM N.A.	FT	DISULFID 47
RC STRAIN=Bangladesh-1975;		FT	DISULFID 68
RX MEDLINE=94089747; PubMed=8264798;		FT	DISULFID 86
RA Massung R.F.; Esposito J.J.; Liu L.; Qi J.; Utterback T.R.;		FT	DISULFID 100
RA Knight J.C.; Aubin L.; Yuran T.E.; Parsons J.M.; Loparev V.N.;		FT	CARBOHYD 101
RA Sejlianov N.A.; Cavallaro K.F.; Kerlavage A.R.; Mahy B.W.J.;		FT	CARBOHYD 173
RA Venter C.J.;		FT	CARBOHYD 189
RT "Potential virulence determinants in terminal regions of variola smallpox virus genome.";		FT	CARBOHYD 215
RL Nature 366:748-751(1993).		FT	CARBOHYD 248
RN [3]	SEQUENCE FROM N.A.	FT	CARBOHYD 249
RC STRAIN=Garcia-1966, and Somalia-1977;		FT	VARIANT 160
RA Massung R.F.; Loparev V.N.; Knight J.C.; Chizhikov V.E.; Parsons J.M.,		FT	VARIANT 165
RA Totmenin A.V.; Shchelkunov S.N.; Esposito J.J.;		FT	VARIANT 182
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.		FT	VARIANT 182
RN [4]	SEQUENCE FROM N.A.	FT	VARIANT 274
RC STRAIN=Garcia-1966;		FT	VARIANT 335
RX MEDLINE=20107289; PubMed=10539322;		FT	VARIANT 339
RA Shchelkunov S.N.; Totmenin A.V.; Loparev V.N.; Safronov P.F.;		FT	SEQUENCE 349 AA:
RA Gutarov V.N.; Chizhikov V.E.; Knight J.C.; Parsons J.M.; Massung R.F.;		FT	38189 MW: D45D4B5CE780EF CRR64;
RT "Alastrim smallpox variola minor virus genome DNA sequences.";		Qy	Query Match 16.3%; Score 257; DB 1; Length 349;
RT Viralology 266:3161-386(2000).		Db	Best Local Similarity 29.3%; Pred. No. 1.8e-13; Indels 42; Gaps 8
RL [5]	SEQUENCE FROM N.A.	Db	Mismatches 66; Conservative Matches 66; Conservative
RA Loparev V.N.; Parsons J.M.; Esposito J.J.;		Qy	21 LRLWLYLTFLIGAPC-----YAPLPSCKEDEYVNGSSEQCPKSPSPGYRKVEACCEL 70
RT "DNA sequence analysis as a criterion for allocation of the orthopoxviruses to a particular species.";		Db	1 MKSIVLYLVLFFSLTNGRDAAPYPTPEPGKCKDTEYKRHNLLCSPGTAVASRICSK 60
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		Qy	71 TGTVCCEPCPGTVTAHLNGLSKCIQCO-MCDPAMGLRASRSNTENAVCGGSPGHFCV 1299
CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes (By similarity).		Db	61 TNTOCTPCGSGITTSRNHLPAGLSCNRCN-SNOVETRSNTTHNRCESPSGPYC 1188
CC -!- SUBCELLULAR LOCATION: secreted (By similarity).		Qy	130 QGDHCAACRAYATSSPCQRVKGGTESQOPTICQNCPGFTS-----PNGLE 1771
CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.		Db	119 KGSSGCKACVSQPRKGIGYGV-SGHTSVGDVICSPPCGFGTYHTVSSADKCERPVNPNTN 1777
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CC	RESULT 9	Db	178 YIDVEITLYPVNDTSCRTTT--TGSES----ITSELITM 214
CC	TNR3_HUMAN	ID	TNR3_HUMAN
DR	STANDARD;	AC	P26941;
EMBL; X69198; CAM49137.1; -	PRT;	DT	01-JUN-1994 (Rel. 29, Created)
DR		DT	01-JUN-1994 (Rel. 29, Last sequence update)
DR		DT	15-SEP-2003 (Rel. 42, Last annotation update)
DR		DE	Tumor necrosis factor receptor superfamily member 3 precursor (lymphotoxin-beta receptor) (tumor necrosis factor receptor 2 related protein) (tumor necrosis factor C receptor).
DR		DE	(Lymphotoxin-beta receptor) (tumor necrosis factor receptor 2 related protein) (tumor necrosis factor C receptor).
DR		GN	LTFBR OR TNFSF3 OR TNFR.
DR		OS	Homo sapiens (Human).
DR		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DR		PIR; D36858; D36858.	

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 >269 POTENTIAL.
FT DOMAIN 20 193 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 5.
FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37 BY SIMILARITY.
FT DISULFID 38 51 BY SIMILARITY.
FT DISULFID 41 59 BY SIMILARITY.
FT DISULFID 62 77 BY SIMILARITY.
FT DISULFID 83 103 BY SIMILARITY.
FT DISULFID 105 119 BY SIMILARITY.
FT DISULFID 111 116 BY SIMILARITY.
FT DISULFID 125 143 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON TER 269 269
SQ SEQUENCE 269 AA; 29983 MW; -746903F30F95F387 CRC64;

Query Match

16.9%; Score 267; DB 1; Length 269;

Best Local Similarity 28.0%; Pred. No. 2.2e-14; Indels 14; Gaps 5; Matches 65; Conservative 43; Mismatches 110; Indels 14; Gaps 5;

QY 20 VIRLVLYLTFLG---APCYAAPALPSCKEDEYPVGSECCPKSPGYRVEAGCBLTGIVCE 76
Db 1 MYRLPIQTLFWGFLAVHSEPAATCGBKQVYNPSLCLCDLCPGQKUWVNDTCIEVKTEQ 60
Qy 77 PCPPGTYIAHLNGLSKCLQOCMCDPAMGLRASRNCSTENAVCGCSPGHFCITVODESDHCA 136
Db 61 SGCGKEFFLSTWNREKYLEHRYCNPNLGIRIASEGTNTDTICVCYEGQHC---TSHTE 117
Qy 137 AGRAYATSSPGQRVQKGCTESQDTLCQCPGTFPS-PNGTLEECQHOTKCSWL-VTKAGA 194
Db 118 SSCPFLSLCPGPGRVQKQIATGLDUTCSPCPGLFSNNSAFFKCHRMTSCERKGQLYEHQV 177
Qy 195 GISSSHWWWWFLSGSLVIVIVESTVGLLICKRKPRGDVVKVIVSVQRQ 246
Db 178 GTNKTDVCGFQSRRMRTLVVPIVTMGVLFAVLL-----VSACIRNITKKRQ 223

RESULT 5
CRMB CAMPs STANDARD; PRT; 349 AA.AC OBUYÄ7; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB Soluble TNF receptor II precursor (cytokine response modifying protein B) (CRMB1 OR CRMP2L OR CMV002) AND (CRMB2 OR CMP205R OR CMV210).

GN Camelpox virus (strain CMS), and Camelpox virus (strain M-96); OS Camelpox virus (strain M-96); OC Viruses; dDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; OC Orthopoxvirus; OC - TaxID:203172, 203173;

RN [1] SEQUENCE FROM N.A.
RP STRAIN-CMS;
RC Pubmed-1107336;
RA Guibet C., Smith G.L.; DE The Sequence of camelpox virus shows it is most closely related to variola virus, the cause of smallpox."; J. Gen. Virol. 83:855-872(2002).
RT [2] SEQUENCE FROM N.A.RN STRAIN-M-96; OS Shope fibroma virus (strain Kasza) (SFV).
RP Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; OC Ieporipoxvirus.
RC NCBI_TaxID=10272;
RA Alonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L., Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L., RA

RT "The genome of camelpox virus.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
FT -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes (By similarity).
CC CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.

CC CC -----
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CC CC -----
DR DR EMBL; AY009089; AAG37718 1; -;
DR DR EMBL; AF438165; AAU73920 1; -;
DR DR EMBL; AF438165; AAU73917 1; -;
DR DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6.
DR SMART; SM00208; TNFR_3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 349 SOLUBLE TNF RECEPTOR II.
FT REPEAT 31 65 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 65 BY SIMILARITY.
FT DISULFID 68 83 BY SIMILARITY.
FT DISULFID 86 100 BY SIMILARITY.
FT DISULFID 90 108 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 349 AA; 38064 MW; EA412AF991E087FF3 CRC64;

Query Match

16.9%; Score 266.5; DB 1; Length 349; Best Local Similarity 33.1%; Pred. No. 3.1e-14; Indels 15; Gaps 5; Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

QY 21 LRLVLYLTFLGAPC-----YARALPSCKEDEYPVGSECCPKSPGYRVEAGCGL 70
Db 1 MKSVSISYLFLSCLTININGRDVTPYRFSNGKCKDNYKRHNLLCUCSPPGTYASRUDSK 60
Qy 71 TGTVCBPCPPGTYIAHLNGLSKCLQQ-MCDPAMGLRASRNCSTENAVCGCSPGHFCIV 129
Db 61 TNTQCPCPGSCTFTSRNNHLTACLSNGRCD---SNVETRSNTNHRICCSPGYCIL 118
Qy 130 QGDGHACRAYATSSPGQRVQKGCTESQDTLCQCPGTFPSN-GTLEECQ 180
Db 119 KGSSGCRACVSOQTKCGIGYGV-SGHTSAGDVICSPCGLGIVSRTVSSADKE 169

RESULT 6
VT2 SVVKA STANDARD; PRT; 325 AA.ID ID P25943; 01-MAY-1992 (Rel. 22, Created)
DT DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT DT 28-FEB-2003 (Rel. 41, Last annotation update)DE Tumor necrosis factor soluble receptor precursor (Protein T2).
GN GN T2.
RN RN Shope fibroma virus (strain Kasza) (SFV).
RP Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; OC Ieporipoxvirus.
RC NCBI_TaxID=10272;
RA RN [1] SEQUENCE FROM N.A.

RT the ligand binding domain of the human B cell receptor CD40.;
 RL Proteins 27:59-70(1997).
 RN [11]

RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
 RX MEDLINE=98266353; PubMed=9605317;
 RA Singh J., Garber E., van Vilim H., Karpusas M., Hsu Y.-M.,
 RT Zheng Z., Naismith J.H., Thomas D.;
 "The role of polar interactions in the molecular recognition of CD40L
 with its receptor CD40.";
 Protein Sci. 7:1124-1135(1998).

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
 TRAF3.;
 RX PubMed=10984535;
 RA Ni C.Z., Welsh K., Leo E., Chiou C.K., Wu H., Reed J.C., ELY K.R.;
 RT "Molecular basis for CD40 signaling mediated by TRAF3.";
 Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).

RN [13]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
 TRAF3.;
 RX PubMed=12005438;
 RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
 Satterthwait A.C., Cheng G., ELY K.R.;
 "Downstream regulator TANK binds to the CD40 recognition site on
 TRAF3.";
 RT Structure 10:403-411(2002).

RL [14]

RP VARIANT HIGM3 ARG-83.
 RX MEDLINE=21532895; PubMed=11675497;
 RA Ferrari S., Gilioli S., Insalaco A., Al-Ghonaium A., Soresina A.R.,
 Loussier M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,
 RA Levy Y., Catalan N., Durandy A., Tbakhri A., Notarangelo L.D.,
 Plebani A.;

RT "Mutations of CD40 gene cause an autosomal recessive form of
 immunodeficiency with hyper IgM.";
 Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).

!-- FUNCTION: Receptor for TNFSF5/CD40L.
 -- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6.
 -- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 Secreted (isoform II).
 -- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=Additional isoforms seem to exist;
 Name=I;
 CC IsoId=P25942-1; Sequence=Displayed;

Name=II;
 CC IsoId=P25942-2; Sequence=VSP_006472, VSP_006473;

!-- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
 --!- DISEASE: Defects in TNFRSF5 are the cause of type 3 hyper-IgM
 immunodeficiency (HIGM), an autosomal recessive disorder which
 includes an inability of B cells to undergo isotype switching, one
 of the final differentiation steps in the humoral immune system,
 an inability to mount an antibody-specific immune response, and a
 lack of germinal center formation.

--!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 --!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
 CC WWW=<http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm>.

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CC DR PDB: 1LOA; 03-FEB-00.
 CC DR PDB: 1CZZ; 26-SEP-01.
 CC DR PDB: 1D00; 31-OCT-01.

Query Match 17.0%; Score 267.5; DB 1; Length 277;
 Best Local Similarity 26.1%; Pred. No. 2e-14; Indels 35; Gaps 9;
 Matches 71; Conservative 50; Mismatches 116;

QY 20 VRLVLYVLTFLGAPCYAPAU----PSCKEDEYVGSECCPKCSPGVRKEACCELTGTV 74
 DB 1 MVRPLQCWLNG--GLTAVHPPEPTACREKQLINSOCCSLCPGOKLVSDETE 58

QY 75 CEPGPPTGYIAHLNGLSKQLCQCMCPANGLRASRNCRTERENAVGCGSPGHFCIVQDHD 134
 DB 59 CLPGCESERFLDTWNRETHCHOKYCDPNLGLRVQKGITSETDTCTCBGBWHC---TSEA 115

QY 135 CAACRAYATSSPGORVKQGEGTESDPLCONCPCFTS PNGTLEBCQHOTKCSW-LVTK 191
 DB 116 CESCVLHRCSPGPGVKQFATGVSDTCBPCPVGFFNSVSSAEKCHWTSCTTKDULVQ 175

QY 192 AGAGTSSSSHWWWWFLSGSLWIVIVCSTVGLIICVKRKRGDVVKVTVSVQRKOEABGE 251
 DB 176 Q-AGTNKTDWVCGQDRDLRALWVPIPTFGILFA-----ILLVLUPIKKVAKKPTNK 225

QY 252 ATVIEALQRPDV-----TTVAVEETI 273
 DB 226 AP--HPKQEQEIQNFPPDDLGGSNTAAAPVQETL 255

RESULT 4

TRN5_BOVIN ID TRN5_BOVIN STANDARD; PRT; 269 AA.
 AC Q28203;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 5 precursor
 DE (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
 GN TNFRSF5 OR CD40.

OS Bos taurus (Bovine).
 OC Bubaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;
 OC Mammalia; Eutheria; Cotariodiactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]

RP SEQUENCE FROM N_A, ID TRN5_BOVIN
 RX MEDLINE=97281252; PubMed=9135560;
 RA Hirano A., Brown W.C., Estes D.M.,
 RT "Cloning, expression and biological function of the bovine CD40
 homologue: role in B-lymphocyte growth and differentiation in
 cattle.";
 RL Immunology 90:294-300(1997).

CC CC --!- FUNCTION: Receptor for TNFSF5/CD40L.
 CC --!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6 (BY
 CC similarity).
 CC --!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC --!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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CC DR EMBL; U57745; AAC48710.1; -.
 CC DR HSSP; P25942; ICDF.
 CC DR InterPro; IPR001368; TNFR_c6.
 CC DR Pfam; PF00020; TNFR_c5; 4.
 CC DR SMART; SM00208; TNFR; 4.
 CC DR PROSITE; PS50050; TNFR_NGFR_2; 1.

DR PROSITE; PS50050; TNFR_NGFR_2; 1.

RESULT 2	
TNFR_MOUSE	PRT: 289 AA.
ID_TNFS_MOUSE	STANDARD; PRT: 289 AA.
AC_P27512; O99NE0; O99NE2; O99NE3;	
DT_01-AUG-1996 (Rel. 23, Created)	
DT_01-OCT-1996 (Rel. 34, Last sequence update)	
DT_15-SEP-2003 (Rel. 42, Last annotation update)	
DE_Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (CDw40).	
DE_CD40L receptor (B-cell surface antigen CD40) (CDw40).	
GN_TNFRSF5 OR CD40.	
OS_Mus musculus (Mouse)	
OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI_TaxID=10090;	
RN_11;	
RP_SEQUENCE FROM N.A. (ISOFORM I).	
RC_MEDLINE=92105763; PubMed=1370315;	
RA_Torres R.M.; Clark E.A.;	
RT_Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.;	
RT_J. Immunol. 148:620-626(1992).	
[2]	
RP_REVISONS.	
RC_STRAIN_BALB/c;	
RA_Torres R.M.;	
RL_Submitted (Sep-1996) to the EMBL/GenBank/DBJ databases.	
[3]	
RP_SEQUENCE FROM N.A. (ISOFORM I).	
RC_STRAIN_BALB/c; TISSUE=liver;	
RA_Grimaldi J.C.; Torres R.; Kozak C.A.; Chang R.; Clark E.A.;	
RA_Howard M.; Cockayne D.A.;	
RT_Genomic structure and chromosomal mapping of the murine CD40 gene.;	
J. Immunol. 149:3921-3926(1992).	
[4]	
RP_SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND V).	
RA_MEDLINE=2117110; PubMed=1172033;	
RA_Tone M.; Tone Y.; Fairchild P.J.; Wykes M.; Waldmann H.;	
RT_Regulation of CD40 function by its isoforms generated through alternative splicing.;	
RL_Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).	
[5]	
RP_INTERACTION WITH TRAF3.	
RA_MEDLINE=95184010; PubMed=7533327;	
RA_Cheng G.; Cleary A.M.; Ye Z.S.; Hong D.I.; Lederman S.; Baltimore D.;	
RT_Involvement of CRAF, a relative of TRAF, in CD40 signaling.;	
RL_Science 267:1494-1498(1995).	
[6]	
RP_INTERACTION WITH TRAF5.	
RA_MEDLINE=96382484; PubMed=8790348;	
RA_Ishida T.; Tojo T.; Aoki T.; Kobayashi N.; Ohishi T.; Watanabe T.;	
RA_Yamamoto T.; Inoue J.-I.;	
RT_TRAF5, a novel tumor necrosis factor receptor-associated factor family protein, mediates CD40 signaling.;	
RT_Proc. Natl. Acad. Sci. U.S.A. 93:9417-9421(1996).	
-!- FUNCTION: Receptor for TNFSF5/CD40L.	
-!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1, TRAF2 AND TRAF6 (BY SIMILARITY).	
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV and V); Secreted (isoform II).	
CC_C and V); Secreted (isoform II).	
CC_ALTERNATIVE PRODUCTS:	
-!- Event=Alternative splicing; Named isoform=5;	
CC_Name=I;	
CC_Isoid=P27512-1; Sequence=Displayed;	
CC_Name=II;	
CC_Isoid=P27512-2; Sequence=VSP_006474, VSP_006475;	
CC_Name=III;	
CC_Isoid=P27512-3; Sequence=VSP_006477, VSP_006478;	
CC_Name=IV;	
CC_Isoid=P27512-4; Sequence=VSP_006479, VSP_006480;	
CC_Name=V;	
CC_Isoid=P27512-5; Sequence=VSP_006476;	
CC_Query Match 17.5%; Score 276.5; DB 1; Length 289;	
CC_Best Local Similarity 27.9%; Pred. No. 4; le-15;	
CC_Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;	
CC_Name=VI;	
CC_Isoid=P27512-6; Sequence=VSP_006481;	
CC_Query Match 17.5%; Score 276.5; DB 1; Length 289;	
CC_Best Local Similarity 27.9%; Pred. No. 4; le-15;	
CC_Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;	
CC_ID_TNFS_MOUSE	-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC_TNFS_MOUSE	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use -by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC_EM93312; AAB08705.1;	
CC_EM94129; AAA37404.1; JOINED.	
CC_EM94128; AAA37404.1; JOINED.	
CC_EM94127; AAA37404.1; JOINED.	
CC_EM9401387; CAC29427.1.	
CC_EM9401388; CAC29428.1.;	
CC_EM9401389; CAC29429.1.;	
CC_EM941390; CAC29430.1.;	
CC_PIR: A46476; A46476.	
DR_RHSP; P25942; 1ICP.	
DR_MGI: 68336; TNFRSF5.	
DR_Interpro; IPR001368; TNFR_c6.	
DR_Pfam; PF00020; TNFR_c6.	
DR_SMART; SMC0208; TNFR_c6.	
DR_PROSITE; PS0050; TNFR_NGFR_2.	
DR_KW_Receptor; Transmembrane; Glycoprotein; Repeat; Signal;	
FT_ALTERNATIVE_splicing 1.19	POTENTIAL.
FT_CHAIN 20 289	TUMOR NECROSIS FACTOR RECEPTOR
FT_DOMAIN 20 193	SUPERFAMILY MEMBER 5.
FT_TRANSMEM 194 215	EXTRACELLULAR (POTENTIAL).
FT_DOMAIN 216 289	CYTOPLASMIC (POTENTIAL).
FT_REPEAT 25 60	TNFR-CYS 1.
FT_REPEAT 61 103	TNFR-CYS 2.
FT_REPEAT 104 144	TNFR-CYS 3.
FT_REPEAT 145 187	TNFR-CYS.
FT_DISULFID 26 37	BY SIMILARITY.
FT_DISULFID 38 51	BY SIMILARITY.
FT_DISULFID 41 59	BY SIMILARITY.
FT_DISULFID 62 77	BY SIMILARITY.
FT_DISULFID 83 103	BY SIMILARITY.
FT_DISULFID 105 119	BY SIMILARITY.
FT_DISULFID 111 116	BY SIMILARITY.
FT_DISULFID 125 143	BY SIMILARITY.
FT_DISULFID 153 203	N-LINKED (GLCNAC -> SEDKNLFLVQKGTSQNVICGKSRVALLIPVVMG -> RIKVDPASPGASCRODCHPHFRGVSLYQKGQETKG -> (in isoform II)).
FT_DISULFID 166 216	(FTId=VSP_006474.
FT_VARSPLIC 204 289	Missing (in isoform II).
FT_VARSPLIC 187 216	(FTId=VSP_006475.
FT_VARSPLIC 216 234	GIKSRMALLVPGVVMGILITFGVFLIXK -> E (in isoform V).
FT_VARSPLIC 235 289	(FTId=VSP_006476.
FT_VARSPLIC 216 222	KKVVKKKRDKNEMLPPAARR -> SECSGEEERGGFPVPEA (in isoform IV).
FT_VARSPLIC 223 289	(FTId=VSP_006477.
FT_VARSPLIC 289 AA; 32111 MW; CRC64;	Missing (in isoform III).
FT_VARSPLIC 216 222	(FTId=VSP_006478.
FT_VARSPLIC 223 289	KKVVKKKRDKNEMLPPAARR -> SECSGEEERGGFPVPEA (in isoform IV).
FT_VARSPLIC 289 AA; 32111 MW; CRC64;	Missing (in isoform IV).
FT_VARSPLIC 216 222	(FTId=VSP_006479.
FT_VARSPLIC 223 289	(FTId=VSP_006480.

RA Raha S.S., Loqueillano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,
 RA Bass S.A., McEwan P.J., McKeman K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
 RA Schnarr A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 DR human and mouse cDNA sequences.";
 DR Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [6]
 RP INTERACTION WITH TRAF2 AND TRAF5.
 RX PubMed=9153189;
 RN RT
 RP RT through TRAF2 and TRAF5.";
 RN J. Biol. Chem. 272:13471-13474 (1997).
 [7]
 RP INTERACTION WITH TRAF3 AND TRAF5.
 RX PubMed=9162022;
 RA Marsters S.A.; Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
 RA Ashkenazi A.;
 RT "Herpesvirus entry mediator, a member of the tumor necrosis factor
 receptor (TNFR) family, interacts with members of the TNFR-associated
 factor family and activates the transcription factors NF-kappaB and
 RT AP-1.";
 RL J. Biol. Chem. 272:14029-14032 (1997).
 RN X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
 RX MEDLINE=21403268; PubMed=11511370;
 RA Carti A., Willis S.H., Whitebeck J.C., Krummenacher C., Cohen G.H.,
 RA Eisenberg R.J., Wiley D.C.;
 RT "Herpes simplex virus glycoprotein D bound to the human receptor
 RVEA.";
 RL Mol. Cell. 8:169-179 (2001).
 CC !- FUNCTION: receptor for TNFSF14/LIGHT and homotrimeric
 TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
 an important role in HSV pathogenesis because it enhanced the
 entry of several wild-type HSV strains of both serotypes into CHO
 cells, and mediated HSV entry into activated human T cells.
 CC !- SUBUNIT: interacts with TRAF2, TRAF3 and TRAF5.
 CC !- SUBCELLULAR LOCATION: Type I membrane protein (probable).
 CC !- TISSUE SPECIFICITY: widely expressed, with the highest expression
 CC in lung, spleen, and thymus.
 CC !- SIMILARITY: contains 3 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
 DR KW 3D-structure.
 DR SIGNAL_ 1 38
 DR CHAIN 39 283
 FT DOMAIN 39 202
 FT TRANSMEM 203 223
 FT DOMAIN 224 283
 FT REPEAT 42 75
 FT REPEAT 78 119
 FT REPEAT 121 162
 FT DISULFID 42 53
 FT DISULFID 54 67
 FT DISULFID 78 93
 FT DISULFID 96 111
 FT DISULFID 99 119
 FT DISULFID 121 138
 FT DISULFID 127 135
 FT CARBOYL 110 110
 FT CARBOYL 173 173
 FT VARIANT 17 17
 FT VARIANT 241 241
 FT TURN 44 45
 FT STRAND 46 46
 FT STRAND 49 49
 FT TURN 50 51
 FT STRAND 52 52
 FT STRAND 55 55
 FT STRAND 57 57
 FT TURN 59 60
 FT STRAND 61 65
 FT STRAND 74 77
 FT TURN 80 81
 FT STRAND 82 83
 FT STRAND 88 88
 FT TURN 94 95
 FT TURN 101 104
 FT STRAND 105 109
 FT STRAND 118 121
 FT TURN 123 124
 FT STRAND 125 129
 FT STRAND 137 140
 SQ SEQUENCE 283 AA; 30392 MW; 46CB13C2C70242C1 CRC64;
 DR -----
 DR Query Match 99.8%; Score 1575; DB 1; Length 283;
 DR Best Local Similarity 99.6%; Pred. No. 1.7e-18;
 DR Matches 282; Conservative 1; Mismatches 0; Gaps 0;
 DR Index 0;
 DR -----
 DR QY 1 MRPPGDWGGPPWRSTRTDVRVLVLYTFLGAPCVADALPSCKEDDPYVGSECCPKCSPG 60
 DR 1 MEPPGDWGGPPWRSTRTDVRVLVLYTFLGAPCVADALPSCKEDDPYVGSECCPKCSPG 60
 DR -----
 DR Db 61 YRVKEAGELTGTVCECPGPYIAHNGSKCLOQMCDAWGLRSNRNSRTENAVCG 120
 DR 61 YRVKEAGELTGTVCECPGPYIAHNGSKCLOQMCDAWGLRSNRNSRTENAVCG 120
 DR -----
 DR QY 121 CSPGHFCIVQDGDCAACRAYATSSPGQRVKGGTESQDTLICCONCPGTSPNGTLEBCQ 180
 DR 121 CSPGHFCIVQDGDCAACRAYATSSPGQRVKGGTESQDTLICCONCPGTSPNGTLEBCQ 180
 DR -----
 DR QY 181 HQTKCSWLVTKAGAGTSSHHWWFLSGSLIVIVIVESTVGLICVKRKPRGDVWKIVS 240
 DR 181 HQTKCSWLVTKAGAGTSSHHWWFLSGSLIVIVIVESTVGLICVKRKPRGDVWKIVS 240
 DR -----
 DR QY 241 VORKRQEAEGETVTELQAPPDVTTVAEEETIPSPTRGRSPNH 283
 DR 241 VORKRQEAEGETVTELQAPPDVTTVAEEETIPSPTRGRSPNH 283
 DR -----
 DR SMART; SM0028; TNFR_c6; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.

GenCore version 5.1.6
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On protein - protein search, using sw model

Run on: November 14, 2003, 17:27:40 ; Search time 17 Seconds
 Sequence: (without alignments) 782.856 Million cell updates/sec

Title: US-08-741-095B-26
 Perfect score: 1578
 Sequence: 1 MPPGDNGPPPWRSTPRDV. VTVAVVBETIPSFTGRSPNH 283

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
 Maximum DB seq length: 280000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1575	99.8	283	1 TR14_HUMAN	Q92956 homo sapien
2	276.5	17.5	289	1 TNR5_MOUSE	P27512 mus musculus
3	267.5	17.0	277	1 TNR5_HUMAN	P25242 homo sapien
4	267.5	16.9	269	1 TNR5_BOVIN	Q82803 bos taurus
5	266.5	16.9	349	1 CRMB_CAMPS	Q8uva1 camelopex vi
6	260	16.5	325	1 TR12_SFYNA	P25243 shope fibro
7	259	16.4	461	1 TR1B_HUMAN	P20333 homo sapien
8	257	16.3	349	1 CRMB_TARV	P34015 variola vir
9	253.	16.0	435	1 TNR3_HUMAN	P36341 homo sapien
10	245.	15.6	300	1 TR6B_HUMAN	Q95007 homo sapien
11	245.5	15.6	415	1 TNR3_MOUSE	P50284 mus musculus
12	243.5	15.4	351	1 CRMB_COWPX	O75599 cowpox virus
13	240.5	15.2	271	1 TRN4_RAT	P15722 rattox norv
14	238.5	15.1	326	1 WT2_MTXVL	P29025 myxoma virus
15	236	15.0	332	1 TNR6_PIG	O77736 sus scrofa
16	215.5	13.7	272	1 TNR4_MOUSE	P47741 mus musculus
17	213.5	13.5	417	1 TR16_MOUSE	Q9zow1 mus musculus
18	213.5	13.5	474	1 TR1B_MOUSE	P25119 mus musculus
19	210	13.3	401	1 T11B_HUMAN	P00300 homo sapien
20	209.5	13.3	616	1 T11_HUMAN	Q9y6q6 homo sapien
21	206.5	13.1	324	1 TNR6_RAT	Q63199 rattus norvegicus
22	206.5	13.1	417	1 TR25_HUMAN	Q9j038 h tumor nec
23	206	13.1	335	1 TNR6_HUMAN	P24445 homo sapien
24	205	13.0	327	1 TNR6_MOUSE	P25446 mus musculus
25	205	13.0	655	1 TR21_HUMAN	O75509 homo sapien
26	204	12.9	401	1 T11B_MOUSE	Q08712 mus musculus
27	203.5	12.9	425	1 TR16_RAT	P07174 rattus norvegicus
28	201	12.7	401	1 T11B_RAT	Q08722 rattus norvegicus
29	200.5	12.7	323	1 TNR6_BOVIN	P51867 bos taurus
30	198.5	12.6	416	1 TR16_CHICK	P18319 gallus gallus
31	198.5	12.6	625	1 TR11_MOUSE	O35305 mus musculus
32	196	12.4	655	1 TR21_MOUSE	Q9epu8 mus musculus
33	194.5	12.3	277	1 TNR4_HUMAN	P43489 homo sapien

ALIGNMENTS

RA	RESULT 1	TR14_HUMAN	ID	TR14_HUMAN	STANDARD; PRT; 283 AA.
AC			AC	Q92956; Q8WXR1; Q9GJ31; Q9UW65;	
DT			DT	16-OCT-2001 (Rel. 40'; Created)	
DT			DT	16-OCT-2001 (Rel. 40'; Last sequence update)	
DT			DT	15-SEP-2003 (Rel. 42'; Last annotation update)	
DE			DE	Tumor necrosis factor receptor superfamily member 14 precursor (Herpesvirus entry mediator A)	(Tumor necrosis factor receptor-like 2)
DE			DE	(TR2).	
GN			GN	Homo sapiens (Human);	
OC			OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo sapiens (Human); Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OCBT_TaxID=9606;	
OX			OX		
RN			RN		
RP			RP	SEQUENCE FROM N.A.	[1]
RT			RT	"Herpes simplex virus-1 entry into cells mediated by a novel member of the TNF-NGF receptor family"; Cell 87:427-436(1996).	[2]
RT			RT		
RT			RT	SEQUENCE FROM N.A.	
RT			RT	Medline:97306336; PubMed=9162061;	
RT			RT	Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J., Wang S., Gantz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C., Porter T.G., Truneh A., Young P.R.;	
RT			RT	A newly identified member of the tumor necrosis factor receptor superfamily with a wide tissue distribution and involvement in lymphocyte activation."; J. Biol. Chem. 272:14272-14276(1997).	
RT			RT	Zhang W., Wan T., Cao X., Zhang W., Wan T., Cao X., Submitted (May-1999) to the EMBL/GenBank/DBJ databases.	[3]
RT			RT	SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.	[4]
RT			RT	Medline:21629477; PubMed=1156919;	
RT			RT	Strynf F., Posavac C.M., Keyaerts E., Van Ranst M., Corey L., Spear P.G.;	
RT			RT	"Search for polymorphisms in the genes for herpesvirus entry mediator, Nectin-1, and Nectin-2 in immune seronegative individuals."; J. Infect. Dis. 185:36-44 (2002).	
RT			RT	Nectin-1, and Nectin-2 in immune seronegative individuals.";	
RT			RT	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stippler M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	

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Qy 50 GSECCPKCSPGYRVKACGELTGTV---CEPCPG---TYIAHLNGSKCLOCQMC 100
Db 56 GQFCHKPCPGERKARDC---TVMGDEPPDCVPCQEGKEYTDKAHFS-SKCRRCRLC 108
Qy 101 PAMGLRASRNRSTEMAVCGSPGHCIVQGDHCAACRAYATSSPGQRVQKGIESQDT 160
|| || || || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 109 EGHGLEVEINCTRONTWKCRCKPNFFC-----NST 138
Qy 116 LQNCPGTFSPNGTLEEC--OHQTKCSWLVTKAGAGTSSSHWWFLSGSLVIVCST 218
|| : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 139 VCEHCOPCTKEHGLIKECTITSNTKC---KEGSRSLIGW-----LCLLIP 183
Qy 219 VGLICCVKRKPRGRGDYKVTVSVORRQEAEGETAELQAPPVTVAEETIPSFQ 278
|| : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 184 IPLIVWVKRK-----VOKTCRKRKENQSHESPTLNPTVAINLSDVUDSKYTTAG 238

Search completed: November 14, 2003, 17:32:18
Job time : 22 secs

Db 71 TSDIVCADCEASMYTQVNQFRCLSCSSCTTDQEYRA--CTKQNRVACEAGRYC 127
 Qy 128 IVO-DGDHCACRAYATSSPQQRVKGGTESQDTLCONCPGTRS - PNGTLEECQHOTKC 185
 Db 128 ALKTHSGSCRQCRMLSKKGPGFVGASSRAPNGNVLCKACAPMSDTSSTDVCPHRIC 187
 Qy 186 SWIUTVKACAGTSS 198
 Db 188 SILAIPGNASTDA 200

RESULT 13
 148854 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C;Accession: I48854
 R;Powell, E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
 Ramm, Genome 5, 726-727, 1994
 A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
 A;Reference number: I48854; MUID:95178848; PMID:787384
 A;Accession: I48854
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-459 <RES>
 A;Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831
 C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology <NGF>
 F;151-188/Domain: NGF receptor repeat homology

Query Match Best Local Similarity 13.1%; Score 206.5; DB 2; Length 324;
 Matches 58; Conservative 27; Mismatches 93; Index 57; Gaps 6;
 Query Match Best Local Similarity 24.7%; Pred. No. 5.7e-08;
 Matches 58; Conservative 27; Mismatches 93; Index 57; Gaps 6;

Db 41 SCKEDEVFPVGSCCPKPKSPGYRKVECGELGT-VCBPCPPG-TYFAHLNGLSKCHQCM 98
 Qy 41 SCKEDEVFPVGSCCPKPKSPGYRKVECGELGT-VCBPCPPG-TYFAHLNGLSKCHQCM 98
 Db 43 NCSEGLYQVGPFCCQCPQPGERKVKDCTTSGGAPTCPCTGEYETDRKHYSDKCCRCAF 102
 Qy 99 CDPAMGRASNSRRENAVGCSPEHFCIQDGDRCAACAYATSSPGQVKSGESQ 158
 Db 103 CDBGHGHEVETNTTRONTKCRKENPYCNASICDCHYHC---TSGGLEDELPCTRTS 158
 Qy 159 DTLCQNCQPGTFSPTSPNGTLECOHQTKCSWLVTKAGACTSSHHWWFLSGSLIVIVCST 218
 Db 159 NTKKKK-----QSNYKLMLUNL-----ILPLG 180
 Qy 219 VGIICVKKRPRGDDVVKVIVSVORKQEAEGATVTEALQAPPDVTVAYETI 273
 Db 181 ATLFVFYK-----YRKQPGDPESGIESPESVPMNVSDVNLYKI 222

RESULT 14
 A40036 apoptosis-mediating surface antigen Fas precursor - human
 N;Alternate names: surface antigen APO-1
 C;Species: Homo sapiens (man)
 C;Date: 17-Jan-1992 #sequence revision 17-Jan-1992 #text_change 21-Jul-2000
 C;Accession: A40036; S24543; A38142
 R;Ittoh, N.; Yonhara, S.; Ishii, A.; Yonhara, M.; Mizushima, S.I.; Sameshima, M.; Hase, Cell 66, 233-243, 1991
 A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis
 A;Reference number: A40036; MUID:91309137; PMID:1713127
 A;Accession: A40036
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-335 <RNA>
 A;Cross-references: GB:M67454; NID:9182409; PIDN:AAA63174.1; PID:9182410
 R;Krammer, P.H.
 Submitted to the EMBL Data Library, February 1992
 A;Reference number: S24543
 A;Accession: S24543
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-335 <RNA>
 A;Cross-references: EMBL:X63717; NID:928741; PID:928742
 R;Oehm, A.; Behmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Ricci, J. Biol. Chem. 267, 10709-10715, 1992
 A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member of the CD45 gene family
 A;Reference number: A38142; MUID:92268122; PMID:1375228
 A;Accession: A38142
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-147, 'Q', 136-335 <OEH>
 A;Experimental source: SKW6.4 cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:103810)
 A;Note: in NCBI backbone the source is designated as mouse
 C;Genetics:
 A;Gene: GDB:AP11
 A;Cross-references: GDB:132671; OMIM:134637
 A;Map Position: 10q4.1-0q24.1
 C;Superfamily: NGF receptor repeat homology
 C;Keywords: apoptosis; surface antigen; transmembrane protein
 F;1-16/Domain: signal sequence #status predicted <SIG>
 F;22-24/Product: Fas antigen #status predicted <MAT>
 F;44-79/Domain: NGF receptor repeat homology <NGF>
 F;174-190/Domain: transmembrane #status predicted <TMM>

Query Match Best Local Similarity 13.1%; Score 206; DB 2; Length 335;
 Matches 60; Conservative 30; Mismatches 82; Index 68; Gaps 9;

Db	122	-CVPCCPGHFS-P-GNNQACKPWNCT	145
RESULT 10			
T2 protein - myxoma virus (strain Lausanne)			
C;Species: myxoma virus			
C;Accession: 31-Dec-1992 #sequence_revision 31-dec-1992 #text_change 18-Jun-1999			
C;Date: 31-Dec-1992			
C;Cross-references: EMBL:KX85214; PIDN:G9732818; PIDN:CAA59476.1; PID:G9732819			
A;Residues: 1-14 ,G' 16-272 <RE2>			
A;Cross-references: EMBL:KX85214; PID:G9732818; PIDN:CAA59476.1; PID:G9732819			
C;Genetics:			
A;Gene: ox40			
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1			
C;Superfamily: CD27 antigen; NGF receptor repeat homology			
Query Match			
Best Local Similarity 13.7%; Score 215.5; DB 2; Length 272;			
Matches 46; Conservative 17; Mismatches 58; Indels 25; Gaps 5;			
C;Species: Mus musculus (mouse)			
C;Accession: A40566			
A;Molecule type: DNA			
A;Residues: 1-326 <UPT>			
A;Cross-references: GB:NM95181; GB:M37976; NID:G9332309; PIDN:AAA46632.1; PID:G9332310			
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology <NG2>			
C;Keywords: glycoprotein			
F;64-105-/Domain: NGF receptor repeat homology <NG2>			
F;106-147-/Domain: NGF receptor repeat homology <NG3>			
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted			
RESULT 11			
Query Match			
Best Local Similarity 15.1%; Score 238.5; DB 1; Length 326;			
Matches 73; Conservative 30; Mismatches 104; Indels 65; Gaps 11;			
C;Species: Mus musculus (mouse)			
C;Accession: B31634			
A;Molecule type: DNA			
A;Residues: 1-474 <LEW>			
A;Cross-references: GB:M6469; NID:G919987; PIDN:AAA39752.1; PID:G9199828			
R;Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Mol. Cell. Biol. 11, 3020-3026, 1991			
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors			
A;Reference number: A38634; MUID:9187885; PMID:1849278			
A;Accession: B31634			
A;Molecule type: mRNA			
A;Residues: 1-474 <GOO>			
A;Cross-references: GB:M6469; NID:G919987; PIDN:AAA39752.1; PID:G9199828			
R;Kissnerchis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.			
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors			
A;Reference number: A40254; MUID:91246166; PMID:1645445			
A;Accession: A40254			
A;Molecule type: mRNA			
A;Residues: 1-474 <GOO>			
A;Cross-references: GB:M6469; NID:G919987; PIDN:AAA39752.1; PID:G9199828			
R;Kissnerchis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.			
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors			
A;Reference number: A40254; MUID:91246166; PMID:1645445			
A;Accession: S54816			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-122 <KIS>			
A;Cross-references: EMBL:Y87128; NID:G980943; PIDN:CAA60618.1; PID:G980944			
C;Species: tumor necrosis factor receptor type 2; NGF receptor repeat homology			
C;Accession: I49700; F48334; S54377			
R;Calderhead, D.M.; Buhmann, J.B.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993			
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interaction			
A;Reference number: I48700; MUID:94047750; PMID:8228223			
A;Accession: I48700			
A;Status: translated from GB/EMBL/DDJB			
A;Molecule type: mRNA			
A;Residues: 1-272 <RES>			
A;Cross-references: EMBL:221674; NID:G912827; PIDN:CAA7972.1; PID:G912828			
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.			
Bur. J. Immunol. 25, 926-930, 1995			
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat Ox40			
A;Reference number: I48334; MUID:95255413; PMID:737295			
A;Accession: I48334			
A;Status: translated from GB/EMBL/DDJB			
A;Molecule type: DNA			
RESULT 12			
Query Match			
Best Local Similarity 13.7%; Score 215.5; DB 2; Length 272;			
Matches 46; Conservative 17; Mismatches 58; Indels 25; Gaps 5;			
C;Species: Mus musculus (mouse)			
C;Accession: B30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999			
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chee, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991			
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors			
A;Reference number: A38634; MUID:9187885; PMID:1849278			
A;Accession: B31634			
A;Molecule type: mRNA			
A;Residues: 1-474 <LEW>			
A;Cross-references: GB:M6469; NID:G919987; PIDN:AAA39752.1; PID:G9199828			
R;Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Mol. Cell. Biol. 11, 3020-3026, 1991			
A;Title: Cloning and expression of the type 1 and type 2 murine tumor necrosis factor receptors			
A;Reference number: A40254; MUID:91246166; PMID:1645445			
A;Accession: A40254			
A;Molecule type: mRNA			
A;Residues: 1-474 <GOO>			
A;Cross-references: GB:M6469; NID:G919987; PIDN:AAA39752.1; PID:G9199828			
R;Kissnerchis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.			
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors			
A;Reference number: A40254; MUID:91246166; PMID:1645445			
A;Accession: S54816			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-122 <KIS>			
A;Cross-references: EMBL:Y87128; NID:G980943; PIDN:CAA60618.1; PID:G980944			
C;Species: tumor necrosis factor receptor type 2; NGF receptor repeat homology			
C;Accession: I49700; F48334; S54377			
R;Calderhead, D.M.; Buhmann, J.B.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993			
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interaction			
A;Reference number: I48700; MUID:94047750; PMID:8228223			
A;Accession: I48700			
A;Status: translated from GB/EMBL/DDJB			
A;Molecule type: mRNA			
A;Residues: 1-272 <RES>			
A;Cross-references: EMBL:221674; NID:G912827; PIDN:CAA7972.1; PID:G912828			
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.			
Bur. J. Immunol. 25, 926-930, 1995			
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat Ox40			
A;Reference number: I48334; MUID:95255413; PMID:737295			
A;Accession: I48334			
A;Status: translated from GB/EMBL/DDJB			
A;Molecule type: DNA			
RESULT 13			
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Best Local Similarity 13.5%; Score 213.5; DB 2; Length 474;			
Matches 55; Conservative 20; Mismatches 101; Indels 17; Gaps 6;			
C;Species: cytokine receptor; transmembrane protein			
C;Accession: I49700; F48334; S54377			
R;F1-22/Domain: signal predictor #status predicted <SIG>			
F;40-77-/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>			
F;40-77-/Domain: NGF receptor repeat homology <NG1>			
F;79-120/Domain: NGF receptor repeat homology <NG2>			
F;166-203/Domain: NGF receptor repeat homology <NG4>			
Query Match			
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Matches 55; Conservative 20; Mismatches 101; Indels 17; Gaps 6;			
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C;Accession: I49700; F48334; S54377			
R;F1-22/Domain: signal predictor #status predicted <SIG>			
F;40-77-/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>			
F;40-77-/Domain: NGF receptor repeat homology <NG1>			
F;79-120/Domain: NGF receptor repeat homology <NG2>			
Query Match			
Best Local Similarity 31.5%; Score 215.5; DB 2; Length 272;			
Matches 46; Conservative 17; Mismatches 58; Indels 25; Gaps 5;			
C;Species: tumor necrosis factor receptor type 2			
C;Accession: B30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999			
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chee, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991			
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors			
A;Reference number: A38634; MUID:9187885; PMID:1849278			
A;Accession: B31634			
A;Molecule type: mRNA			
A;Residues: 1-474 <LEW>			
A;Cross-references: GB:M6469; NID:G919987; PIDN:AAA39752.1; PID:G9199828			
R;Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Mol. Cell. Biol. 11, 3020-3026, 1991			
A;Title: Cloning and expression of the type 1 and type 2 murine receptors			
A;Reference number: A40254; MUID:91246166; PMID:1645445			
A;Accession: S54816			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-122 <KIS>			
A;Cross-references: EMBL:Y87128; NID:G980943; PIDN:CAA60618.1; PID:G980944			
C;Species: cytokine receptor; transmembrane protein			
C;Accession: I49700; F48334; S54377			
R;F1-22/Domain: signal predictor #status predicted <SIG>			
F;40-77-/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>			
F;40-77-/Domain: NGF receptor repeat homology <NG1>			
F;79-120/Domain: NGF receptor repeat homology <NG2>			
Query Match			
Best Local Similarity 31.5%; Score 215.5; DB 2; Length 272;			
Matches 46; Conservative 17; Mismatches 58; Indels 25; Gaps 5;			
C;Species: tumor necrosis factor receptor type 2			
C;Accession: B30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999			
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chee, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991			
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors			
A;Reference number: A40254; MUID:91246166; PMID:1645445			
A;Accession: S54816			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-122 <KIS>			
A;Cross-references: EMBL:Y87128; NID:G980943; PIDN:CAA60618.1; PID:G980944			
C;Species: cytokine receptor; transmembrane protein			
C;Accession: I49700; F48334; S54377			
R;F1-22/Domain: signal predictor #status predicted <SIG>			
F;40-77-/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>			
F;40-77-/Domain: NGF receptor repeat homology <NG1>			
F;79-120/Domain: NGF receptor repeat homology <NG2>			

RESULT 7

D36858

gene G4R protein - variola virus

N;Alternate names: B28R protein (COP)

C;Species: variola virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001

C;Accession: D36858; S46888; S32385; S35987

R;Blinov, V.M.

R;Submitter: to GenBank, November 1992

A;Reference number: A36859

A;Accession: D36858

A;Molecule: preliminary

A;Residues: 1-449 <BLI>

A;Cross-references: GB:X69198; NID:9456758; PIDN:CAA49137.1; PID:9457087

A;Experimental source: strain India-1967, ssp. major, isolate Ind3

R;Koikhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol submitted to the EMBL Data Library April 1992

A;Description: Nucleotide sequence analysis of the region of Variola virus Xhol P O H P

A;Reference number: S46858

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-449 <KOI>

A;Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA7540.1; PID:9516449

A;Experimental source: strain India-1967, isolate Ind3

R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhtchiev, L.S.

PEBS Lett. 319, 80-83, 1993

A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A;Reference number: S32385; MUID:9320281; PMID:8384129

A;Accession: S32385

A;Molecule type: DNA

A;Residues: 31-168 <SHC>

A;Cross-references: EMBL:X69198

A;Experimental source: strain India-1967, ssp. major

C;Genetics:

A;Gene: G4R

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology <NGF>

F;32:66/Domain: NGF receptor repeat homology <NGF>

F;68-109/Domain: NGF receptor repeat homology <NGF>

F;110-151/Domain: NGF receptor repeat homology <NGF>

Query Match

Best Local Similarity 16.3%; Score 257; DB 2; Length 349;

Matches 29.3%; Pred. No. 1.3e-11; Indels 66; Gaps 8; Conservative 23; Mismatches 94;

Db

1 BLRVLYITFLGAPC-----YADALPCKEDEYPVGSBCCPKCSPGIVKEACGEL 70

1 MKSVLVYIYLFLSCITINGRDAAPYPPNGRKDKTEYKRHNLLCLSCPPIGYIASRLCDSK 60

Db

71 TGTVCBPCPPGTYIAHNGSKLOQ-MCPAMGLARASMRNSRTENAVCCSPSGHFCIV 129

61 TWWQTPCGSGFTTSRNHLAPACLSNCGRN--SNQEVTRSNTTHNRICLCPSPGYCIL 118

Db

130 QDGDHCAACRAYATSSFGQRVKGGTESQDILCQNPGGTS-----PNGLIE 177

Db

119 KSSGSKRACVSVQTKGIGYGV-SGHTSVGDVICSPGFGTYSHTVSADKEPVPRNTEN 177

Db

178 ECQ-----HQTCSWLVTKAGTSSSSHVWWFLSGSTVIVI 214

Db

178 YIDVEITLYPMDTSCRTT--TGLES---ILTSETITM 214

Query Match

Best Local Similarity 15.2%; Score 240.5; DB 2; Length 271;

Matches 34.9%; Pred. No. 1.6e-10; Indels 51; Conservative 51; Mismatches 16; Gaps 5;

Db

1 SCKEDDPYVSEBCCPKCSPGIVKEACGEL-TGTVCBPCPPGTYIAHNGSKLOQCMCD 100

Db

25 NCVKDTPPSGHKCRCBQPGHGMVRQDHTRTDVCHCEPGFYNSAWN-YDTCKOCTQCN 83

Db

101 PAMGLARASMRNSRTENAVCCSPSGHFCIVDGPHCACRAYATSSFGQRVKGGTESQD 160

Db

84 HRSGSLKQNPPTDTCOCPG-TOPRODSH-----KLGD---- 121

A;Accession: 154182

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-435 <RES>

A;Cross-references: GB:1.04270; NID:9339761; PIDN:AAA36757.1; PID:9339762

A;Genetics:

A;Gene: GB:LIBR

A;Map position: 12p13.3-12p13.1

A;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C;Query Match

Best Local Similarity 16.0%; Score 253; DB 2; Length 435;

Matches 26.7%; Pred. No. 3e-11; Indels 72; Gaps 16; Conservative 37; Mismatches 127;

Db

4 PG-DWGPFPWRSTPRTDVLRLVLYLETFL-----GAPCYAPALFSCK-BDEY-PVNGS 51

Db

10 PGLANCP-----LVLGFGLLALASQPAVPPASENQTCRDRDEKEYVEPPQR 56

Db

52 ECPKGSPPGIVKEACGELGTGTCBCCPVGTYIAHNGSKLOQCMCDPANGLBRASRN 111

Db

57 ICCSRCPGPYIVSAKSRRDTCATCAENSYNEHWNLNYTICOLCRCPDPWGLEBIA 116

Db

112 SRTENAVGGSPGPHECTVQGDHCACRAVATSSG-----QRYQGGTESQDTLQNC 165

Db

117 TSKRKTQCRCPGMFCAW-ALECTHOELLSDCPGTCATEBLKDEVGKNNH-----CVPC 170

Db

166 PPGTF---SPNGTLEBCQHOTKC-SWLNTKGAGTSSHHWW-----FLSGSLVI 212

Db

171 KAGHFTNTSSPSA---RCQHTRCENQGIVYEACTPQSQTICKPLEPLPPEMGSTM 227

Db

213 VIVCSTVGLIT-----CVYRKPRGQDGVVKVIVSVQRKQEAEGEATVTEALQAD--- 261

Db

228 LAVLLPLAFLILLATVFCIWKSHP-SLCRKUGSILKRRPQGEFPNPVAGSWEPKA 285

Db

262 --PDVTTVATEETISFTGSP 281

Db

286 YFPDL---VQPLLPISGDVSP 303

RESULT 9

S12783

OX40 antigen precursor - rat

N;Alternate names: nerve growth factor receptor homolog

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C;Accession: S12783; S08036

A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte

B;Mallett, S.; Possamai, S.; Barclay, A.N.

EMBO J. 9, 1065-1068, 1990

A;Reference number: S12783; MUID:90214614; PMID:2157591

A;Accession: S12783

A;Molecule type: mRNA

A;Residues: 1-271 <MAT>

A;Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831

A;Superfamily: CD27 antigen; NGF receptor repeat homology

C;Keywords: growth factor receptor; transmembrane protein

F;1-19/Domain: Signal sequence #status predicted <SIG>

F;20-271/Product: OK40 antigen #status predicted <MAT>

F;211-235/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 15.2%; Score 240.5; DB 2; Length 271;

Matches 34.9%; Pred. No. 1.6e-10; Indels 51; Conservative 51; Mismatches 16; Gaps 5;

Db

1 SCKEDDPYVSEBCCPKCSPGIVKEACGEL-TGTVCBPCPPGTYIAHNGSKLOQCMCD 100

Db

25 NCVKDTPPSGHKCRCBQPGHGMVRQDHTRTDVCHCEPGFYNSAWN-YDTCKOCTQCN 83

Db

101 PAMGLARASMRNSRTENAVCCSPGHTCIVDGPHCACRAYATSSFGQRVKGGTESQD 160

Db

84 HRSGSLKQNPPTDTCOCPG-TOPRODSH-----KLGD---- 121

A;Reference number: 154182; MUID:93252381; PMID:8486360

Nature 366, 748-751, 1993
 A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
 A;Reference number: 220488; MUID:94088747; PMID:8264798
 A;Accession: T28623
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-348 <MAS>
 A;Cross References: EMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:9439102
 A;Experimental source: strain Bangladesh 1975
 C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query	Match	Score	Length
Qy	Best local similarity 29.5%; Conservatve 23;	25.5;	348;
Qy	Matches 66; Conservative 23; Mismatches 94; Indels 41; Gaps 8;	Pred. No. 1.2e-11;	
Qy	21 LRLVLYILTFGAPC-----YAPALPSCKEDDEYPVGSECCPKCSPGYRVKREAGELT 71	21	
Db	1 MKSILYLNLFLSCLINGRDAAPTPPPNGKCKOTEYKRHNLLCLSCPPETYASRLCDSKT 60	1	
Qy	72 GTVCEPPCPGTYIHLNGLSKLCQQ-WCDPAMGLASRNRCSRTENAVCGCSPGHFCIVQ 130	72	
Db	61 NTQCTPGCGSTFTSRNNHLPACLSNGRCN-SNOVETRSNTNHRICECSPGYCYLKK 118	61	
Qy	131 DGDHGACRAYATSSPGQRVQKGCTESQDITLQNCPGPTF-----PNGTLEE 178	131	
Db	119 GSSGCKACVSVQTKGGIGKCV-SGHTSVGDVICSPCGFGCHYSHTVSADKCEPVPNNTENY 177	119	
Qy	179 CQ-----HOTKCSWLVTKAGAGTSSHHWWWFLLSGSLIVIVI 214	179	
Db	178 IDVEITLYVPNDISCTRIT--TGLES-----LTISBLTMM 213	178	

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RESULT 15
 AAY05797 DT 02-AUG-1999 (first entry)
 ID AAY05797 standard; protein; 283 AA.
 XX AC AAY05797;
 XX DE Herpes virus entry mediator (HVEM).
 XX KW Herpes virus entry mediator; HVEM; HSV receptor; infection;
 KW diagnosis; therapy; vaccine; antiviral; assay.
 OS Human herpes simplex virus.
 XX PN WO9920761-A2.

Qy 241 WORKQEAEATVIEALQAPPDVTTAEEETISFTGSPNH 283
 Db * 241 WORKQEAEATVIEALQAPPDVTTAEEETISFTGSPNH 283

Search completed: November 14, 2003, 17:30:21
 Job time : 42 secs

XX PD 29-APR-1999.
 XX PF 22-OCT-1998; 98WO-US22342.
 XX PR 22-OCT-1997; 97US-0955531.
 XX PA (UNNMI) UNIV MICHIGAN.
 XX PI Fuller AO, Li Q, McLaren NC, Perez A, Subramanian G;
 XX DR WPI; 1999-302740/25.
 DR N-PDB; AX25512.
 XX PT Human herpes simplex virus receptor B5 and HVEM compositions
 XX PS Claim 10; Page 71-72; 89pp; English.

CC The present sequence represents HVEM, a novel human herpes simplex virus (HSV) entry mediator that is a member of the tumour necrosis factor receptor family, and which confers on HSV the ability to infect and replicate in otherwise non-permissive cells. In the present invention, the combination of a novel porcine cell model system which is refractory to HCV entry, along with specific HSV B5 (see AAY05796), and/or HVEM receptor proteins enables the development of assays for screening antiviral compounds and therapeutics. The assays are useful for detecting the ability of agents to inhibit HSV entry or spread and provide for facile high-throughput screening of compounds suspected to be able to inhibit such entry, e.g. compound libraries, peptide libraries etc., to identify potential drug candidates. The invention also provides a vaccine comprising the HSV receptor, an immunogenic polypeptide or fragments of the polypeptide.

SQ Sequence 283 AA;

Query Match 99.5%; Score 1570; DB 20; Length 283;
 Best local similarity 99.3%; Pred. No. 5.9e-120;
 Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPEPDWGPWRSPRTDVLRLVLYLTFGARCPYAPALPSCKEDEYPVGSECPKCPG 60
 Db 1 MEPPDWGPWRSPRTDVLRLVLYLTFGARCPYAPALPSCKEDEYPVGSECPKCPG 60
 Qy 61 YRKVEACGELTGTVCEPCPGTYIAHNGISKCLQCOMDPAMGLRATRNCSTENAVCG 120
 Db 61 YRKVEACGELTGTVCEPCPGTYIAHNGISKCLQCOMDPAMGLRATRNCSTENAVCG 120
 Qy 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRQKGGETESQTLCONCPPGTFSPTLRCQ 180
 Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRQKGGETESQTLCONCPPGTFSPTLRCQ 180
 Qy 181 HOTKCSWLVYKAGATSSSWWWFLSGSIVIVCSTWGLICVKRKRRKGDVVKVS 240
 Db 181 HOTKCSWLVYKAGATSSSWWWFLSGSIVIVCSTWGLICVKRKRRKGDVVKVS 240

PT useful for treating stroke, Alzheimer's disease and AIDS
 XX disclosure; Page 13-14; 18pp; English.

PS The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 candidate compound in the presence of TL2 or TL4; or (ii), contacting TL2
 or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
 assessing the ability of the candidate compound to compete with TR1 or
 TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
 for treating diseases caused by imbalance of TL or TR polypeptide levels,
 which cause: chronic and acute inflammation, arthritis, septicemia,
 autoimmune diseases, transplant rejection, graft vs. host disease,
 infection, stroke, ischemia, acute respiratory disease syndrome,
 restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis
 and Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TR2.

XX SQ Sequence 283 AA;

Query Match 99.6%; Score 1572; DB 20; Length 283;
 Best Local Similarity 99.6%; Pred. No. 4.1e-120;
 Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MEPPGDWGPWPRSTPRTDVLRLVLYLTLFIGACPYAPALPSCKEDEYPVGSECPKCSPG 60
 1 MEPPGDWGPWPRSTPRTDVLRLVLYLTLFIGACPYAPALPSCKEDEYPVGSECPKCSPG 60

Qy 61 YRVEKACGELGTGVCEPCCPGTYIAHNLSKLCIQCQMDPAMGLRASRNCSRTENAVCG 120
 61 YRVEKACGELGTGVCEPCCPGTYIAHNLSKLCIQCQMDPAMGLRASRNCSRTENAVCG 120

Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKGGTESQDTLCONCOPPGTFSPNGTLEBCQ 180
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKGGTESQDTLCONCOPPGTFSPNGTLEBCQ 180

Qy 181 HQTKCSWLVTKAGAGTSSHHWVWFSLGSLSLVIIVCSTVGLICVKRRKPRGDVVKVIVS 240
 181 HQTKCSWLVTKAGAGTSSHHWVWFSLGSLSLVIIVCSTVGLICVKRRKPRGDVVKVIVS 240

Db 241 VQRKQEARGEATVIEAQAPPDVTTVAEETIPSFGRSPNH 283
 241 VQRKQEARGEATVIEAQAPPDVTTVAEETIPSFGRSPNH 283

Qy 241 VQRKQEARGEATVIEAQAPPDVTTVAEETIPSFGRSPNH 283
 241 VQRKQEARGEATVIEAQAPPDVTTVAEETIPSFGRSPNH 283

RESULT 14
 AAW12659
 ID AAW12659 standard; Protein; 283 AA.
 XX
 AC AAW12659;
 XX
 DT 07-MAY-1997 (first entry)

DE Human herpes simplex virus cellular mediator.

XX Herpes simplex virus cellular mediator.

OS Homo sapiens.

XX
 FH Location/Qualifiers
 FT Peptide 1..38 /label= Sig_peptide
 FT Protein 39..283 /label= Mat_protein
 FT Region 42..75 /note= "cysteine-rich repeat characteristic of TNF/NGF receptor family"
 FT Region 76..120 /note= "cysteine-rich repeat characteristic of TNF/NGF receptor family"
 FT Region 121..162

XX SQ Sequence 283 AA;

Query Match 99.5%; Score 1570; DB 18; Length 283;
 Best Local Similarity 99.3%; Pred. No. 5.9e-120;
 Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MEPPGDWGPWPRSTPRTDVLRLVLYLTLFIGACPYAPALPSCKEDEYPVGSECPKCSPG 60
 1 MEPPGDWGPWPRSTPRTDVLRLVLYLTLFIGACPYAPALPSCKEDEYPVGSECPKCSPG 60

Qy 61 YRVEKACGELGTGVCEPCCPGTYIAHNLSKLCIQCQMDPAMGLRASRNCSRTENAVCG 120
 61 YRVEKACGELGTGVCEPCCPGTYIAHNLSKLCIQCQMDPAMGLRASRNCSRTENAVCG 120

Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKGGTESQDTLCONCOPPGTFSPNGTLEBCQ 180
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKGGTESQDTLCONCOPPGTFSPNGTLEBCQ 180

Qy 181 HQTKCSWLVTKAGAGTSSHHWVWFSLGSLSLVIIVCSTVGLICVKRRKPRGDVVKVIVS 240
 181 HQTKCSWLVTKAGAGTSSHHWVWFSLGSLSLVIIVCSTVGLICVKRRKPRGDVVKVIVS 240

Db 241 VQRKQEARGEATVIEAQAPPDVTTVAEETIPSFGRSPNH 283
 241 VQRKQEARGEATVIEAQAPPDVTTVAEETIPSFGRSPNH 283

Db 241 VQRKQEARGEATVIEAQAPPDVTTVAEETIPSFGRSPNH 283

	Best Local Similarity	100.0%	Pred.	No.	1.3e-120;	Matches	283;	Conservative		Mismatches	0;	Indels	0;	Gaps	0;	
QY	1	MEPPGDWGPWRSTPRTDVLRLVLYTFLGACPYAPALPSCKEDEYNGSECQPKCSPG	60			CC		receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that selectively binds to the TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide.								
Db	1	MEPPGDWGPWRSTPRTDVLRLVLYTFLGACPYAPALPSCKEDEYNGSECQPKCSPG	60			CC		The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein.								
QY	61	YRVKEACGELGTGTVCECPGTYIAHNGSKLCQMCQCDPAMGLRASRSRTEAVCG	120			CC										
Db	61	YRVKEACGELGTGTVCECPGTYIAHNGSKLCQMCQCDPAMGLRASRSRTEAVCG	120			CC										
QY	121	CSPGHCTIVQGDHCAACRAYATSSGQRVKGGTESQDTLQNCQCPGTTSPNGTLECO	180			CC										
Db	121	CSPGHCTIVQGDHCAACRAYATSSGQRVKGGTESQDTLQNCQCPGTTSPNGTLECO	180			CC										
QY	181	HOTKCSWLTKAGGTSSSHWWFLGSLSLVIVCSTVGLIICVRKPRGRDVVKIVS	240			CC										
Db	181	HOTKCSWLTKAGGTSSSHWWFLGSLSLVIVCSTVGLIICVRKPRGRDVVKIVS	240			CC										
QY	241	VORKQEAEGEATVIEALQAPPDVTVAVEETIPSFTGRSPNH	283			CC										
Db	241	VORKQEAEGEATVIEALQAPPDVTVAVEETIPSFTGRSPNH	283			CC										
RESULT 9																
ID	ABU0681	standard; Protein; 283 AA.				Query Match	100.0%	Score	1578;	DB	24;	length	283;			
XX						Best Local Similarity	100.0%	Pred.	No.	1.3e-120;	Mismatches	0;	Indels	0;	Gaps	0;
AC	ABU0681;					Matches	283;	Conservative								
XX																
DT	06-MAY-2003	(first entry)														
DE	Human membrane-bound Herpesvirus Entry Mediator (mHVERM).															
XX																
KW	Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HVEM; SHVEM1; SHVEM2; mHVERM; tumour necrosis factor receptor; TNFR; immune disorder; autoimmune disorder; arthritis; graft rejection; T-cell disorder; AIDS; inflammatory disorder; bacterial infection; psoriasis; septicemia; cerebral malaria; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder; asthma; psoriasis; apoptotic disorder; rheumatic arthritis; systemic lupus erythematosus; insulin-dependent diabetes mellitus; cytotoxic disorder; septic shock; cachexia; proliferative disorder; B-cell cancer.					QY	1	MEPPGDWGPWRSTPRTDVLRLVLYTFLGACPYAPALPSCKEDEYNGSECQPKCSPG	60			CC				
Db						Db	1	MEPPGDWGPWRSTPRTDVLRLVLYTFLGACPYAPALPSCKEDEYNGSECQPKCSPG	60			CC				
QY	61	YRVKEACGELGTGTVCECPGTYIAHNGSKLCQMCQCDPAMGLRASRSRTEAVCG	120			Db	61	YRVKEACGELGTGTVCECPGTYIAHNGSKLCQMCQCDPAMGLRASRSRTEAVCG	120			CC				
Db						Db	121	CSPGHCTIVQGDHCAACRAYATSSGQRVKGGTESQDTLQNCQCPGTTSPNGTLECO	180			CC				
QY	121	CSPGHCTIVQGDHCAACRAYATSSGQRVKGGTESQDTLQNCQCPGTTSPNGTLECO	180			Db	121	CSPGHCTIVQGDHCAACRAYATSSGQRVKGGTESQDTLQNCQCPGTTSPNGTLECO	180			CC				
Db						Db	181	HOTKCSWLTKAGGTSSSHWWFLGSLSLVIVCSTVGLIICVRKPRGRDVVKIVS	240			CC				
QY	181	HOTKCSWLTKAGGTSSSHWWFLGSLSLVIVCSTVGLIICVRKPRGRDVVKIVS	240			Db	181	HOTKCSWLTKAGGTSSSHWWFLGSLSLVIVCSTVGLIICVRKPRGRDVVKIVS	240			CC				
QY	241	VORKQEAEGEATVIEALQAPPDVTVAVEETIPSFTGRSPNH	283			Db	241	VORKQEAEGEATVIEALQAPPDVTVAVEETIPSFTGRSPNH	283			CC				
Db																
RESULT 10																
AAW60045						Query Match	100.0%	Score	1578;	DB	24;	length	283;			
ID	AAW60045	standard; Protein; 283 AA.				Best Local Similarity	100.0%	Pred.	No.	1.3e-120;	Mismatches	0;	Indels	0;	Gaps	0;
XX						Matches	283;	Conservative								
AC	AAW60045;															
XX																
DT	25-SEP-1998	(first entry)														
XX																
DE	Human TNF receptor related (TR2) protein.															
XX																
KW	Human; tumour necrosis factor; TNF; herpes simplex virus; aberrant cell survival; radiation therapy; lymphocyte proliferation; immune deficiency syndrome.															
XX																
OS	Homo sapiens.															
XX																
FH	Key location/qualifiers															
FT	Peptide 1..36															
FT	/note= "Signal peptide"															
FT	Peptide 37..283															
FT	/note= "Mature peptide"															
FT	37..200															
FT	Domain /note= "Extracellular domain"															
FT	Modified-site 110															
FT	/note= "Asparagine-linked glycosylation site"															
FT	Modified-site 173															
FT	/note= "Asparagine-linked glycosylation site"															

Disclosure; Fig 10; 79pp; English.

The invention relates to an isolated nucleic acid molecule, designated as New TANGO-69 receptor polynucleotides and polypeptides, useful for treating arthritis, graft rejection, AIDS, bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, asthma, psoriasis, lupus - disclosure; Fig 10; 79pp; English.

CC TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion of the proteins SHVEM1, SHVEM2, and mHVERM (where HVERM is a Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a

membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that selectively binds to the TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis), septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein.

CC membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that selectively binds to the TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis), septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein.

CC membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that selectively binds to the TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis), septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein.

KW Human; tumour necrosis factor receptor; TNFR-Galpha; TNFR-6beta; therapy;
 KW immune system-related disorder; inflammatory disease; immunosuppressive;
 KW bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;
 KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
 KW multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;
 KW graft versus host disease; GVHD; anti-inflammatory; psoriasis; arthritis;
 KW neuroprotective; antiarteriosclerotic; dermatological; asthma.
 OS Homo sapiens.
 XX PN WO200218622-A2.
 XX PD 07-MAR-2002.
 XX PR 24-AUG-2001; 2001WO-US26395.
 XX PR 25-AUG-2000; 2000US-227598P.
 PR 21-NOV-2000; 2000US-252131P.
 PR 06-JUL-2001; 2001US-303224P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Gentz RL, Ebner R, Yu G, Ruben SM, Ni J, Feng P;
 XX DR WPI; 2002-281068/32.
 XX Novel nucleic acid molecules comprising a polynucleotide encoding human
 PT tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides
 PT useful for treating disease e.g. inflammatory and autoimmune disorders
 PT XX Claim 36; Page 346-347; 350pp; English.
 XX The invention relates to human tumour necrosis factor receptor (TNFR)-
 CC 6alpha and 6beta protein and their corresponding nucleic acids. The
 CC invention provides screening methods for identifying agonists and
 CC antagonists of TNFR-6alpha and 6beta activity. The invention also
 CC provides diagnostic and therapeutic methods for detecting and treating
 CC immune system-related disorders. The method is useful for treating or
 CC preventing an inflammatory disease or disorder selected from bowel
 CC disease,encephalitis, atherosclerosis and psoriasis, an autoimmune
 CC disease or disorder selected from systemic lupus erythematosus,
 CC arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
 CC and autoimmune encephalitis, graft versus host disease (GVHD), and an
 CC allergy or asthma. The present sequence is human TNFR-Galpha and TNFR-
 XX sequence 283 AA;
 SQ 100.0%; Score 1578; DB 23; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1..3e-120; Mismatches 0; Indels 0; Gaps 0;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSPPGDKCPPPRSPTRPTDVLRLVLYTFLGAPCYAPALPSCKEDEPVGSRCCPKKSPG 60
 Db 1 MEPPGDWGPWRSPTRPTDVLRLVLYTFLGAPCYAPALPSCKEDEPVGSRCCPKKSPG 60
 Qy 61 YRKKEACELTGIVCECPPPGTYIAHLNGLKLQLCQCMCDPAMGLRASRNRSRTENAVCG 120
 Db 61 VTKAEAGELTGIVCECPPGTVAHNGLKLQCOMCDPAMGLRASRNRSRTENAVCG 120
 Qy 121 CSPGHFCITQDGDHCAACRAYATSSPGORVQKGTEQDTLCONCPGTFSPNGTBEQ 180
 Db 121 CSGFHFCIVQDGDHCAACRAYATSSPGORVQKGTEQDTLCONCPGTFSPNGTBEQ 180
 Qy 181 HOPKCSWLVTKACAGTSSHHWWFLCSLIVIIVTCCTVGLLICVKERKPRDVVKIVS 240
 Db 181 HOPKCSWLVTKACAGTSSHHWWFLCSLIVIIVTCCTVGLLICVKERKPRDVVKIVS 240
 Qy 241 VOKRQEAEGETAIEALQAPPVTTVAETIPSGFGRSPNH 283
 Db 241 VOKRQEAEGETAIEALQAPPVTTVAETIPSGFGRSPNH 283
 XX Sequence 283 AA;
 Query Match 100.0%; Score 1578; DB 24; Length 283;
 RESULT 8
 ABR40215 standard; Protein; 283 AA.
 ID ABR40215
 XX AC ABR40215;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human cobesin.
 XX OS Homo sapiens.
 XX Human; coesin; lipid partitioning; lipid metabolism; weight reduction;
 KW insulin-like activity; free fatty acid oxidation; anorectic; antilipemic;
 KW antiarteriosclerotic; antidiabetic; hypotensive; immunomodulator;
 KW cytostatic; anti-HIV; antiinflammatory; antidepressant; weight loss;
 KW obesity.
 XX OS Homo sapiens.
 XX PH Key Peptide Location/Qualifiers
 FT Peptide 1..38
 FT Protein /label= Signal_peptide
 FT Domain 39..283
 FT Domain /label= Mature_cobesin
 FT Domain 39..202
 FT Domain /label= Extracellular_domain
 FT Domain 203..223
 FT Domain /label= Transmembrane_domain
 FT Domain 224..283
 FT Domain /label= Intracellular_domain
 XX WO2003011321-A1:
 XX PD 13-FEB-2003.
 XX PR 29-JUL-2002; 2002WO-1B03408.
 PR 31-JUL-2001; 2001US-309233P.
 XX PA (GEST) GENSET SA.
 XX PT Lucas J, Dialyas D, Briggs K;
 XX DR WPI; 2003-247866/25.
 DR N-PSDB; A8299577.
 XX PT Screening for an agonist or an antagonist of coesin activity, useful
 PT for reducing body mass, maintaining weight loss, or preventing or
 PT treating an obesity-related disease or disorder, e.g. hyperlipidemia,
 PT diabetes or hypertension.
 XX Example 10; Page 34; 37pp; English.
 XX The invention relates to a novel method for screening for an agonist or
 CC an antagonist of coesin activity, i.e. lipid partitioning, lipid
 CC metabolism, insulin-like activity, free fatty acid oxidation, or weight
 CC reduction. The method of the invention has anorectic, antihypertensive,
 CC antiarteriosclerotic, antidiabetic, hypotensive, immunomodulator,
 CC cytostatic, anti-HIV, antiinflammatory, and antidepressant activity. The
 CC method is useful for screening for an agonist or antagonist of coesin
 CC activity. The agonists or antagonists are useful for reducing body mass,
 CC maintaining weight loss, preventing or treating an obesity-related
 disease or disorder, e.g. hyperlipidemia, atherosclerosis, insulin
 CC resistance, diabetes or hypertension. The compounds are also useful for
 CC increasing body mass or treating disorders associated with excessive
 weight loss, e.g. cachexia, cancer-related weight loss, acquired
 CC immunodeficiency syndrome (AIDS)-related weight loss, chronic
 CC inflammatory disease-related weight loss or anorexia. The present
 sequence represents the human coesin of the invention.
 XX Sequence 283 AA;
 Query Match 100.0%; Score 1578; DB 24; Length 283;

treatment of arthritis or inflammation using an antibody directed against a fragment of the TR2 protein. TR2 its agonists, antagonists and antibiotics exhibit cytostatic, dermatological, antianæmic, immunosuppressive, antiallergic, antiarthritic, antiasthmatic, antiinflammatory, neuroprotective, notropic, antiparkinsonian, and cerebroprotective activity. The methods are useful for treating arthritis or inflammation, cancer (such as follicular lymphomas, carcinoma with p53 mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an immunodeficiency or for enhancing an in vivo leukocyte response to an antigen. Anti-TR2 antibodies are useful for treating, inhibiting or preventing autoimmune diseases (such as autoimmune haemolytic anaemia, dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and inflammatory myopathies) and immunodeficiency disorders (such as severely combined immunodeficiency (SCID) X linked, B cell lymphoproliferative disorder, or Nezelot syndrome-combined immunodeficiency with IgS). TR2, TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancers. They are also used to activate, differentiate or proliferate cancerous cells or tissues, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease, Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful as sources for generating antibodies, as molecular weight markers. This sequence represents the TR2 receptor protein of the invention.

卷之三

sequence 203 nm;

```

Query Match      100.0%; Score 1578; DB 21; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.3e-120;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

RESULT 5
 AAY93695
 ID AAY93695 standard; protein; 283 AA.
 XX
 AC
 AAY93695;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE Amino acid sequence of novel polypeptide PRO09.
 XX
 KW PRO201; PRO292; PRO327; PRO1265; PRO343; PRO347; PRO357;
 PRO15; PRO1017; PRO1112; PRO509; PRO834; PRO882; tumour cell;
 tumorigenesis; cancer; neoplastic cell growth; cell proliferation..
 KW

Os

Key location/Qualifiers

FT Peptide 1..36

		RESULT 3
Qy	AAY06488	AAY06488 standard; Protein; 283 AA..
ID	AAV06488	
XX		
AC	AAY06488;	
XX		
DT	27-SEP-1999	(first entry)
XX		
DE	Human tumour-associated protein PRO509.	
XX		
KW	PRO112; UNQ555; cancer; tumour necrosis factor receptor; diagnosis; therapy; human.	
XX		
OS	Homo sapiens.	
XX		
FH		
FT		
Key	Location/Qualifiers	
Domain	201..225 /note= "transmembrane domain" 226..283 /note= "cytoplasmic domain"	
FT		
XX		
PN	W09935170-A2.	
XX		
PD	15-JUL-1999.	
XX		
PF	05-JAN-1999;	
XX	99WO-US00106.	
PR	20-NOV-1998;	98US-0109304.
PR	05-JAN-1998;	98US-0070440.
PR	29-APR-1998;	98US-0083500.
PR	22-MAY-1998;	98US-0086414.
PR	10-JUN-1998;	98US-0088742.
PR	10-NOV-1998;	98US-0107783.
PA	(GETH) GENENTECH INC.	
XX		
PT	Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;	
XX	Roy MA, Wood WI;	
XX		
WPI; 1999-430385/36.		
DR	N-PSDB; AAX87265.	
XX		
PT	Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment	
XX		
PS	Example 1; Fig 24; 162pp; English.	
XX		
CC	This sequence represents human PRO509 (UNQ329); a protein encoded by the novel cDNA clone DNA50148 (see AAX87264), and a member of the tumour necrosis factor receptor family. Amplification of DNA50148 was observed in various tumour tissues, suggesting a role in tumour formation or growth. Antagonists (e.g. antibodies) directed to PRO509 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claimed cancer diagnostic kits.	
CC		
CC		
SQ	Sequence 283 AA;	
Query	Match 100%; Score 1578; DB 20; Length 283;	
Best Local Similarity 100.0%; Pred. No. 1.3e-120;		
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
1 MPPGDMOPPPRSPTRDVLRLVLYLTFLGPCYAPALPSCKEDEYPVGSACCCKSPG 60		
1 MEPPGDMOPPPRSPTRDVLRLVLYLTFLGPCYAPALPSCKEDEYPVGSACCCKSPG 60		
XX		
PS Disclosure; Page 370; 373pp; English.		
CC This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor (TNF)-receptor related protein TR2. Included in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2. The TR2 gene is located on chromosome 1 at position p36.2-p35.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the		
61 YRVKEAGELGTIVCCEPPPGTYIAHLNLKSCLCQCOMCDPAMGLRASRNCSRTENAVCG 120		
181 HQTCKSMLVTKAAGTSSHHWWPLSSLVLTIVCSTVGLICVKKRPRGVVVKIVS 240		
181 HQTCKSMLVTKAAGTSSHHWWPLSSLVLTIVCSTVGLICVKKRPRGVVVKIVS 240		
121 CSPSHFCIVODGDCAACRAYATSSPGORVOKSGCTESOPTLCONCPGGTFSPNPTLEECO 180		
121 CSPSHFCIVODGDCAACRAYATSSPGORVOKSGCTESOPTLCONCPGGTFSPNPTLEECO 180		
241 VQRKRQEAEGETVIAQAPDVTTVAEVETIPSFGRSPNH 283		
Db	241 VQRKRQEAEGETVIAQAPDVTTVAEVETIPSFGRSPNH 283	
Db	RESULT 4	
ID	AAY94721	
XX	AAY94721 standard; Protein; 283 AA.	
XX		
AC	AAY94721;	
XX		
DT	29-JAN-2001 (first entry)	
XX		
DE	Human TR2-receptor protein sequence.	
XX		
KW	Tumour necrosis factor-receptor related protein; TR2; human; cancer; chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.	
XX		
OS	Homo sapiens.	
XX		
FH		
FT		
Key	location/Qualifiers	
Peptide	1..38 /note= "Signal peptide" 39..283 /label= "TR2 receptor"	
FT		
Protein		
FT		
XX		
PN	W0200056405-A2.	
XX		
PD	28-SEP-2000.	
XX		
PF	22-MAR-2000; 2000WO-US07521.	
XX		
PR	22-MAR-1999; 99US-0125683.	
PR	26-MAR-1999; 99US-0126522.	
PR	20-MAY-1999; 99US-0135169.	
PR	06-AUG-1999; 99US-0147383.	
XX		
PA	(NIJJ/) NI J.	
PA	(ROSE/) ROSEN C A.	
PA	(ROSE/) ROSEN C A.	
PA	(GENT/) GENTZ R L.	
XX		
NI J, Rosen CA, Gentz RL;		
XX		
DR	WPI; 2000-94519/56.	
DR	N-PSDB; AAM28149.	
XX		
PT	Nucleic acid molecule encoding a human tumor necrosis factor receptor 2 and its two splice variants, useful for treating arthritis or inflammation, and its two splice variants, useful for treating cancer (such as follicular lymphomas) and immunodeficiency disorders -	
PT		
PT		
PS Disclosure; Page 370; 373pp; English.		
CC This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor (TNF)-receptor related protein TR2. Included in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2. The TR2 gene is located on chromosome 1 at position p36.2-p35.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the		

PF 27-APR-1995; 95WO-US05058.
 XX
 PR 27-APR-1995; 95WO-US05058.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz R, Ni J, Rosen CA;
 XX
 DR WPI; 1996-497627/49.
 DR N-PSDB; AT&T0048.

XX
 PT New nucleic acid encoding a human tumour necrosis factor receptor -
 PT useful for treatment of auto:immune diseases etc., in diagnosis and
 PT for drug screening
 XX
 PS Claim 1; Pages 47-48; 73pp; English.

XX
 CC The present sequence is the human tumour necrosis factor (TNF) receptor, which may be used for the identification of TNF receptor agonists or antagonists. TNF receptor agonists inhibit tumor growth, stimulate cell (e.g. T cell) differentiation, mediate the immune and antiviral responses, regulate growth, protect against radiation and Chlamydia infection, and can be used to treat immunodeficiencies, e.g. human immunodeficiency virus. Antagonists can be used to treat T cell mediated autoimmune disease, inflammation, septic shock, cerebral malaria, cachexia or B cell cancers, to inhibit graft-host reactions and to prevent apoptosis or cytotoxicity. Fragments of the TNF receptor encoding DNA can be used as hybridization probes for detecting related genes.

CC antibodies against the protein can be used as reagents for detecting/measuring soluble forms of protein in the circulation.

XX
 SQ Sequence 283 AA;

Query Match Similarity 100.0%; Score 1578; DB 17; Length 283;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MEPPGDKGPPRSPTRTDVLRLVLYITFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60
 Db 1 MEPPGDKGPPRSPTRTDVLRLVLYITFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60

Oy 61 YRKVEAGELGTGVCECOPPGTYIAHNLGSKLCQCMCDPAMGLRASRNRSRTENAVCG 120
 Db 61 YRKVEAGELGTGVCECOPPGTYIAHNLGSKLCQCMCDPAMGLRASRNRSRTENAVCG 120

Oy 121 CSPGHFCIVQDGHCACRAYATSSPGQRVKGGTESDTLQNCOPPGTFSPNGTLECOQ 180
 Db 121 CSPGHFCIVQDGHCACRAYATSSPGQRVKGGTESDTLQNCOPPGTFSPNGTLECOQ 180

Oy 181 HOTKCSWLVTKAGAGTSSHHWWFLSGSLVIVIVCSTVGLICVKRKPRGDVVKIVS 240
 Db 181 HOTKCSWLVTKAGAGTSSHHWWFLSGSLVIVIVCSTVGLICVKRKPRGDVVKIVS 240

Oy 241 VORKRQEAEGVTEVALQAPPDVTVAVETIPSFGRSRPNH 283
 Db 241 VORKRQEAEGVTEVALQAPPDVTVAVETIPSFGRSRPNH 283

RESULT 2

AAW6938
 ID AAW69238 standard; Protein; 283 AA.
 AC AAW6938;
 XX
 DT 21-OCT-1998 (first entry)

XX
 DE Herpesvirus entry mediator protein.

XX
 KW Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;
 KW gene expression regulator; cellular stress; inflammatory response;
 KW lymphocyte activity regulator; autoimmune response.

XX

OS Homo sapiens.
 XX
 WO9825967-A1.
 PN
 XX
 PD 18-JUN-1998.
 XX
 PF 05-DEC-1997; 97WO-US22278.
 XX
 PR 12-DEC-1996; 96US-0032705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Marsters SA;
 XX
 DR WPI; 1998-348457/30.
 DR N-PSDB; AAV44852.

XX
 PT Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in assays for HVEM and to produce antibodies and transgenic animals, e.g. for drug screening
 XX
 PS Claim 1; Fig 1; 46pp; English.

CC This sequence is the herpesvirus entry mediator (HVEM) protein of the invention. The protein is useful in quantitative diagnostic assays for HVEM, in affinity purification of HVEM from recombinant cells/natural sources, and in competitive-type receptor binding assays. It can also be used to generate antibodies, also useful in diagnostic assays for HVEM and affinity purification of HVEM. HVEM is believed to be a member of the tumour necrosis factor receptor (TNFR) family, and transient transfection of HVEM into human 293 cells caused marked activation of certain transcription factors, e.g. AP-1, suggesting that HVEM is involved in regulating gene expression in response to infectious stimuli and cellular stress. The predominant expression of HVEM mRNA in lymphocyte-rich tissues (e.g. spleen and peripheral blood) also suggested it may be a receptor in regulating lymphocyte activity. Antibodies produced may therefore be useful therapeutically, e.g. antagonistic antibodies may be useful to block excessive inflammatory/autoimmune response resulting from e.g. Ap-1 induction, whilst agonistic antibodies may enhance HVEM regulation of such induction. The DNA may be used diagnostically, e.g. to determine if DNA and/or RNA encoding HVEM is present in cells, and to prepare HVEM polypeptide recombinantly. It is also useful to produce non-human transgenic animals (e.g. mice or rats), especially knockout animals containing cells with an altered gene encoding HVEM polypeptide. Such animals are useful in the development and screening of therapeutically useful reagents.

XX
 SQ Sequence 283 AA;

Query Match Similarity 100.0%; Score 1578; DB 19; Length 283;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MEPPGDKGPPRSPTRTDVLRLVLYITFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60

Oy 61 YRKVEAGELGTGVCECOPPGTYIAHNLGSKLCQCMCDPAMGLRASRNRSRTENAVCG 120
 Db 61 YRKVEAGELGTGVCECOPPGTYIAHNLGSKLCQCMCDPAMGLRASRNRSRTENAVCG 120

Oy 121 CSPGHFCIVQDGHCACRAYATSSPGQRVKGGTESDTLQNCOPPGTFSPNGTLECOQ 180
 Db 121 CSPGHFCIVQDGHCACRAYATSSPGQRVKGGTESDTLQNCOPPGTFSPNGTLECOQ 180

Oy 181 HOTKCSWLVTKAGAGTSSHHWWFLSGSLVIVIVCSTVGLICVKRKPRGDVVKIVS 240
 Db 181 HOTKCSWLVTKAGAGTSSHHWWFLSGSLVIVIVCSTVGLICVKRKPRGDVVKIVS 240

Oy 241 VORKRQEAEGVTEVALQAPPDVTVAVETIPSFGRSRPNH 283
 Db 241 VORKRQEAEGVTEVALQAPPDVTVAVETIPSFGRSRPNH 283

ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/041,886
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 2626
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-041-886-27

Query Match 17.0%; Score 267.5; DB 3; Length 276;
 Best Local Similarity 26.1%; Prcd. No. 2.1e-16;
 Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;
 Qy 20 VRLVLYLTFLGAPCYAPALL----PSCKEDEYPVGSSBCCPKCSPGVRVKACGELGTGV 74
 Db 1 WRLPLQCVLWG---CLLTAVHREPPATCREKYLINSQCCSLCQPGOKLVSDCTETETE 58
 Qy 75 CEPCPGRTYIAHLNLGSKLCQCOMCDPAMGLRASRNNSRTHENAVCGSPGPFCIVODGDH 134
 Db 59 CLPGGESEBFDTWNRETHCHQHKYCDPNIGLRVQKGSETDTCTCBEGHHC--TSEA 115
 Qy 135 CAACRAVATSPGQRYQKGTSQDTCQNCPCPGTS-PNGPLECOHQTCWS--LVTK 191
 Db 116 CBSCVLRSCPGFGVKQIATGVSDTCEPCPVGFPSNVSSAFEKHPWTSCTKDILVQ 175
 Qy 192 AGAGTSSSHWWMFLSGSLVTVIVCSTVGLLICVKRRKPRGDVKITIVSVORKRQAEAE 251
 Db 176 Q-AGTNKTDVUGQPDRLRAIWVPIIFGILIA-----ILLUVIFIKRKAKRPTNK 225
 Qy 252 ATVIEALQAPPDV-----TTVAVEETI 273
 Db 226 AP--HPKOEPQEINFPPDDLPGSNTAAPVOETL 255

Search completed: November 14, 2003, 17:32:51
 Job time : 22 secs

US-09-146-950-20
; Sequence 20, Application US/09146950A
; Patent No. 6,287,808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO: 20
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-146-950-20

Query Match 53.2%; Score 839; DB 3; Length 159;
Best Local Similarity 98.0%; Pred. No. 4.8e-68; Mismatches 0; Indels 2; Gaps 1;
Matches 146; Conservative 1; ;
QY 39 LPSCKEDEYPVGSECCPKCSSGIRVKEACGELITGVCEPPPGTVIAHNLGSKLQCOM 98
Db 1 LPSCKEDEYPVGSECCPKCSSGIRVKEACGELITGVCEPPPGTVIAHNLGSKLQCOM 60
QY 99 CDPAMGLRASRNCSRTEANAVAGCSPGHFCTVQDGHCACRAYATSSPGORVQKGTESO 158
Db 61 CDPAMGLRASRNCSRTEANAVAGCSPGHFCTVQDGHCACRAYATSSPGORVQKGTESO 120
QY 159 DTLCONCPGPFPSPNGTLECOHQTNW 187
Db 121 DTLCONCPGPFPSPNGTLECOHQTNW 147

RESULT 13
US-09-146-950-25
; Sequence 25, Application US/09146950A
; Patent No. 6,287,808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 25
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-146-950-25

Query Match 17.5%; Score 276.5; DB 3; Length 289;
Best Local Similarity 27.9%; Pred. No. 3.4e-17; Mismatches 69; Indels 43; Gaps 106; Conservative 43; ;
Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;
QY 41 SCKEDDEYPVGSECCPKCSSGIRVKEACGELITGVCEPPPGTVIAHNLGSKLQCOMD 100
Db 25 TCSDKQYLHDGQCDLQCGPSRLTSHTCALEKTOCHPCDSGEFSAQMRNREIRCHOHRIHE 84
QY 101 PAMGIRASRNCSRTEANAVAGCSPGHFCTVQDGHCACRAYATSSPGORVQKGTESQDT 160
Db 85 PNQDLRKKEGTASDVTCKSGQHCTSKD--CEAQHTCIPGGEMENATETRDT 141
QY 161 LCQNCPGPFPSPNGTLECOHQTNW 215
Db 142 VCHRCPGVGSNSQSLFEKCPYPTSCDKNLEVLQK--GTSQTNVIGLKSRMALIVI 198
QY 216 CSTVGLILIC-----VRK--RKRPGDVKVTVWSORKRQEAEATVTEALQAPPDTT 266
Db 199 PVVWGLILITFGVFLYIKKVKKPDRN--EMLPAPAARRQDPQEME-----DYPGINTA 249
QY 267 VAWBETI 273
Db 250 APYQBT 256

RESULT 14
US-09-041-886-27
; Sequence 27, Application US/09041886
; Patent No. 6,233,872
; GENERAL INFORMATION:
; APPLICANT: Bredeisen, Dale E.
; APPLICANT: Rabideau, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS: 72

RESULT 15
US-09-041-886-27
; Sequence 27, Application US/09041886
; Patent No. 6,233,872
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: Busfield, Samantha J.

NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 7
 LENGTH: 419
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-631-780-7

Query Match 68.0%; Score 1073; DB 4; Length 419;
 Best Local Similarity 100.0%; Pred. No. 1.5e-88; Indels 0; Gaps 0;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPPCDWGPWPRSPRTDVLVLYLTFGAPCYAPALPSCKEDEPVGSECCPKCSPG 60
 Db 1 MEPPCDWGPWPRSPRTDVLVLYLTFGAPCYAPALPSCKEDEPVGSECCPKCSPG 60

Qy 61 YRVKEACGELGTGTCPCPGTYIAHNGLSKLOQCMCDPAMGLRASNRSTENAVCG 120
 Db 61 YRVKEACGELGTGTCPCPGTYIAHNGLSKLOQCMCDPAMGLRASNRSTENAVCG 120

Qy 121 CSPGHFCIVODGDHCAACRAYATSSPGQRVKGGTESQDTLCQNCPGTFSPNGTLEECQ 180
 Db 121 CSPGHFCIVODGDHCAACRAYATSSPGQRVKGGTESQDTLCQNCPGTFSPNGTLEECQ 180

Qy 181 H0TKC 185
 Db 181 H0TKC 185

RESULT 9
 US-09-146-950-2
 Sequence 2, Application US/09146950A
 ; Patent No. 6287808
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
 ; FILE REFERENCE: 09404/05001
 ; CURRENT FILING DATE: 1998-09-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 67.7%; Score 1068; DB 3; Length 193;
 Best Local Similarity 98.4%; Pred. No. 1.6e-88; Indels 0; Gaps 0;
 Matches 184; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEPPCDWGPWPRSPRTDVLVLYLTFGAPCYAPALPSCKEDEPVGSECCPKCSPG 60
 Db 1 MEPPCDWGPWPRSPRTDVLVLYLTFGAPCYAPALPSCKEDEPVGSECCPKCSPG 60

Qy 61 YRVKEACGELGTGTCPCPGTYIAHNGLSKLOQCMCDPAMGLRASNRSTENAVCG 120
 Db 61 YRVKEACGELGTGTCPCPGTYIAHNGLSKLOQCMCDPAMGLRASNRSTENAVCG 120

Qy 121 CSPGHFCIVODGDHCAACRAYATSSPGQRVKGGTESQDTLCQNCPGTFSPNGTLEECQ 180
 Db 121 CSPGHFCIVODGDHCAACRAYATSSPGQRVKGGTESQDTLCQNCPGTFSPNGTLEECQ 180

Qy 181 H0TKC 187
 Db 181 H0TKC 187

RESULT 10
 US-09-146-950-18
 Sequence 18, Application US/09146950A
 ; Patent No. 6287808

Query Match 67.2%; Score 1060; DB 3; Length 197;
 Best Local Similarity 98.4%; Pred. No. 8.6e-80; Indels 2; Gaps 1;
 Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

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 Db 1 MEPPGWGPWPRSPRTDVLVLYLTFGAPCYAPALPSCKEDEPVGSECCPKCSPG 60

Qy 61 YRVKEACGELGTGTCPCPGTYIAHNGLSKLOQCMCDPAMGLRASNRSTENAVCG 120
 Db 61 YRVKEACGELGTGTCPCPGTYIAHNGLSKLOQCMCDPAMGLRASNRSTENAVCG 120

Qy 121 CSPGHFCIVODGDHCAACRAYATSSPGQRVKGGTESQDTLCQNCPGTFSPNGTLEECQ 180
 Db 121 CSPGHFCIVODGDHCAACRAYATSSPGQRVKGGTESQDTLCQNCPGTFSPNGTLEECQ 180

Qy 181 H0TKC 187
 Db 181 H0TKC 187

RESULT 11
 US-09-146-950-4
 Sequence 4, Application US/09146950A
 ; Patent No. 6287808
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
 ; FILE REFERENCE: 09404/05001
 ; CURRENT FILING DATE: 1998-09-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 53.7%; Score 847; DB 3; Length 155;
 Best Local Similarity 98.0%; Pred. No. 8.8e-69; Indels 0; Gaps 0;
 Matches 146; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 39 LPSCCKEDEPVGSECCPKCSCGIRVKEACGELGTGTCPCPGTYIAHNGLSKLOQCM 98
 Db 1 LPSCCKEDEPVGSECCPKCSCGIRVKEACGELGTGTCPCPGTYIAHNGLSKLOQCM 98

Qy 99 CDPMGLRASNRSTENAVCGSPGHFCIVODGDHCAACRAYATSSPGQRVKGGTESQ 158
 Db 61 CDPMGLRASNRSTENAVCGSPGHFCIVODGDHCAACRAYATSSPGQRVKGGTESQ 120

Qy 159 DTLCONCPGTFSPNGTLEECQH0TKC 187
 Db 121 DTLCONCPGTFSPNGTLEECQH0TKC 149

RESULT 12

STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60501

COMPUTER READABLE FORM:
 MEDIUM: TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/12374
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Northrup, Thomas E.
 REGISTRATION NUMBER: 33,268
 REFERENCE DOCKET NUMBER: NOR3446P020PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 616-5400
 TELEX: --
 FAX: (312) 616-5460

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 283 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-12374-2

Query Match 99.5%; Score 1570; DB 5; Length 283;
 Best Local Similarity 99.3%; Pred. No. 2e-133; Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDWQPPWRSPTRDVLRLVLYTFLGARCYAPALPSCKEDEVPGSACCPKSPG 60
 Db 1 MEPPGDWQPPWRSPTRDVLRLVLYTFLGARCYAPALPSCKEDEVPGSACCPKSPG 60

QY 61 YRVEKEAGELTGTVCERPCCPGTYIAHNLGLSKLCQCDPAMGLRASRNCRTENAVCG 120
 Db 61 YRVEKEAGELTGTVCERPCCPGTYIAHNLGLSKLCQCDPAMGLRASRNCRTENAVCG 120

QY 121 CSPGHFCIVQDGHCAACRAYATSSPGORVQKGGETSQDTLQCNCPGTFSPNGTLEBCQ 180
 Db 121 CSPGHFCIVQDGHCAACRAYATSSPGORVQKGGETSQDTLQCNCPGTFSPNGTLEBCQ 180

QY 181 HQTKC 185
 Db 181 HQTKC 185

RESULT 7
 US-09-333-279-7
 Sequence 7, Application US/09333279
 Patent No. 6303336
 GENERAL INFORMATION:
 APPLICANT: SPEAR, Patricia G.
 APPLICANT: MONTGOMERY, Rebecca I.
 TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 CURRENT APPLICATION NUMBER: US/09/333, 279
 CURRENT FILING DATE: 1999-06-15
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 7
 LENGTH: 419
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-333-279-7

Query Match 68.0%; Score 1073; DB 4; Length 419;
 Best Local Similarity 100.0%; Pred. No. 1.5e-88; Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDWQPPWRSPTRDVLRLVLYTFLGARCYAPALPSCKEDEVPGSACCPKSPG 60
 Db 1 MEPPGDWQPPWRSPTRDVLRLVLYTFLGARCYAPALPSCKEDEVPGSACCPKSPG 60

QY 61 YRVEKEAGELTGTVCERPCCPGTYIAHNLGLSKLCQCDPAMGLRASRNCRTENAVCG 120
 Db 61 YRVEKEAGELTGTVCERPCCPGTYIAHNLGLSKLCQCDPAMGLRASRNCRTENAVCG 120

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 Db 121 CSPGHFCIVQDGHCAACRAYATSSPGORVQKGGETSQDTLQCNCPGTFSPNGTLEBCQ 180

QY 181 HQTKC 185
 Db 181 HQTKC 185

RESULT 6
 US-09-509-024-7
 Sequence 7, Application US/08509024B
 Patent No. 6221207
 GENERAL INFORMATION:
 APPLICANT: SPEAR, Patricia G.
 APPLICANT: MONTGOMERY, Rebecca I.
 TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 FILE REFERENCE: 0290-1
 CURRENT APPLICATION NUMBER: US/08/509, 024B
 CURRENT FILING DATE: 1995-07-25
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 7
 LENGTH: 419
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-509-024-7

RESULT 8
 US-09-631-780-7
 Sequence 7, Application US/09631780
 Patent No. 6573058
 GENERAL INFORMATION:
 APPLICANT: SPEAR, Patricia G.
 APPLICANT: MONTGOMERY, Rebecca I.
 TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 FILE REFERENCE: 0290-1
 CURRENT APPLICATION NUMBER: US/09/631, 780
 CURRENT FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: US/08/509, 024B
 PRIOR FILING DATE: 1995-07-25

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2003, 17:29:30 ; Search time 21 Seconds

Title: US-08-741-095B-26

Perfect score: 1578

Sequence: 1 MPPGDWGPWRSTPRTDV..... VTVAVSETIPSFTGRSPNH 283

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 328717 sqs, 42310558 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	1578	100.0	283	4 US-09-333-279-2
3	1578	100.0	283	4 US-09-631-780-2
4	1572	99.6	283	4 US-09-072-993C-2
5	1570	99.5	283	5 PGT-US96-13374-2
6	1073	68.0	419	3 US-08-509-024-7
7	1073	68.0	419	4 US-09-333-779-7
8	1073	68.0	419	4 US-09-631-780-7
9	1068	67.7	193	3 US-09-146-50-2
10	1060	67.2	197	3 US-09-146-50-18
11	847	53.7	155	3 US-09-146-50-4
12	839	53.2	159	3 US-09-146-50-20
13	365	23.1	77	3 US-09-146-50-25
14	276	17.5	289	3 US-09-042-785A-11
15	267.5	17.0	276	3 US-09-041-86-27
16	267.5	17.0	277	3 US-09-042-785A-10
17	267.5	17.0	277	4 US-09-06-153A-10
18	267.5	17.0	277	4 US-09-114-94D-2
19	267.5	17.0	277	4 US-09-573-86-10
20	267.5	17.0	277	4 US-08-338-775A-2
21	260	16.5	207	3 US-09-974-022-47
22	260	16.5	207	3 US-08-795-445A-47
23	260	16.5	207	3 US-08-795-445A-47
24	260	16.5	207	3 US-08-974-186-47
25	260	16.5	207	3 US-08-975-446B-47
26	260	16.5	207	4 US-08-706-945D-133
27	16.5	325	1 US-08-292-549-2	

ALIGNMENTS

RESULT 1

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; Sequence 2, Application US/08509024B
; Patent No. 6291307
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; ATTORNEY: MONTGOMERY, Rebecca I.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/08-509, 024B
; CURRENT FILING DATE: 1995-07-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-509-024-2

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Query Match 100.0%; Score 1578; DB 3; Length 283;
Best Local Similarity 100.0%; Score 1578; DB 3; Length 283;
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Db 1 MPPGDWGPWRSTPRTDVLRLVLYLFLGAPCYPAIPSCKEDEYPVGSECCPKCSPG 60

QY 61 YRKVEACGELGTGTVCECPGTYIAHNLGSKCHQCMDPAMGLRASRNCSRTEAVCG 120
Db 61 YRKVEACGELGTGTVCECPGTYIAHNLGSKCLQCQCDPAMGLRASRNCSRTEAVCG 120

QY 121 CSPGFCTIVQDGICAACTAYATSSPGQRVQKGCTESDTLCNCPCGTFSPNQTLBECQ 180
Db 121 CSPGFCTIVQDGICAACTAYATSSPGQRVQKGCTESDTLCNCPCGTFSPNQTLBECQ 180

QY 181 HQTCKSWLVIKAGACTSSHHWWMFLSSLVIVVVCSTVGLICCVKRRPRGDVVKVIVS 240
Db 181 HQTCKSWLVIKAGACTSSHHWWMFLSSLVIVVVCSTVGLICCVKRRPRGDVVKVIVS 240

QY 241 VORKREQAEATVIEALQAPPDTVTAVEETIPSFTGRSPNH 283
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QY 241 WORKRQEABGEATVIEALQAPPDTVTAVEETIPSFTGRSPNH 283
Db 241 WORKRQEABGEATVIEALQAPPDTVTAVEETIPSFTGRSPNH 283

RESULT 2

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; Sequence 2, Application US/09333279
; Patent No. 6303336
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 14, 2003, 17:30:26 ; Search time 175 Seconds

(without alignments)

1471.469 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578

Sequence: 1 MEPPGDPGPPPWRSRTPRTDV.....VITVAVETIPSFTGRSPNH 283

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Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match

Maximum Match

Listing first

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 21: /cgm2_6/prodata/1/paa/us097A_COMB.pep:/*
 22: /cgm2_6/prodata/1/paa/us097B_COMB.pep:/*
 23: /cgm2_6/prodata/1/paa/us098_COMB.pep:/*
 24: /cgm2_6/prodata/1/paa/us099A_COMB.pep:/*
 25: /cgm2_6/prodata/1/paa/us099B_COMB.pep:/*
 26: /cgm2_6/prodata/1/paa/us099_COMB.pep:/*
 27: /cgm2_6/prodata/1/paa/us01_COMB.pep:/*
 28: /cgm2_6/prodata/1/paa/us02_COMB.pep:/*
 29: /cgm2_6/prodata/1/paa/us03_COMB.pep:/*
 30: /cgm2_6/prodata/1/paa/us04_COMB.pep:/*
 31: /cgm2_6/prodata/1/paa/us06_COMB.pep:/*
 32: /cgm2_6/prodata/1/paa/us0_COMB.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1578	100.0	283	PCT-US01-26396-31

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

```
RESULT 1
PCT-US01-26396-31
; Sequence 31, Application PC/TUS0126396
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PFS54PCT3
; CURRENT APPLICATION NUMBER: PCT/US01/20396
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/1303, 224
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/252, 131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227, 598
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; Query Match
; 100.0%; Score 1578; DB 1; Length 283;
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Matches 283; Conservative 100.0%; Pred. No. 7.2e-19; Best Local Similarity 100.0%; Score 1578; DB 1; Length 283;

Query Match 100.0%; Score 1578; DB 1; Length 283;
 Best Local Similarity 100.0%; Pred. No. 7.2e-119; Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: Azar, Daniel
 APPLICANT: Gish, Kurt C.
 APPLICANT: Hevezi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Wilson, Keith E.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 Title Reference: 018501-002710PCT
 CURRENT APPLICATION NUMBER: PCT/US02/29560
 CURRENT FILING DATE: 2025-11-01
 PRIOR APPLICATION NUMBER: US 60/323,469
 PRIOR FILING DATE: 2001-09-17
 NUMBER OF SEQ ID NOS: 412
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 288
 LENGTH: 283
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 2
 Sequence 288, Application PC/TUS0229560
 PCT-US02-29560-288
 GENERAL INFORMATION:
 APPLICANT: Azar, Daniel
 APPLICANT: Gish, Kurt C.
 APPLICANT: Hevezi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Wilson, Keith E.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 Title Reference: 018501-002710PCT
 CURRENT APPLICATION NUMBER: PCT/US02/29560
 CURRENT FILING DATE: 2025-11-01
 PRIOR APPLICATION NUMBER: US 60/323,469
 PRIOR FILING DATE: 2001-09-17
 NUMBER OF SEQ ID NOS: 412
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 288
 LENGTH: 283
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 3
 Sequence 48, Application PC/TUS0310956
 PCT-US03-10956-48
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 TITLE OF INVENTION: Antibodies that Specifically Bind to TL5
 FILE REFERENCE: PFS81PCT
 CURRENT APPLICATION NUMBER: PCT/US03/10956
 CURRENT FILING DATE: 2003-04-01
 PRIORITY CLAIM:
 PRIORITY APPLICATION NUMBER: 60/312,087
 PRIORITY FILING DATE: 2002-04-15
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 48
 LENGTH: 283
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 4
 Sequence 2, Application PC/TUS9505058
 PCT-US95-05058-2
 GENERAL INFORMATION:
 APPLICANT: NI, ET AL.
 TITLE OF INVENTION: Tumor Necrosis Factor Receptors
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARZILLA, BYRNE, BAIN, GILFILLAN,
 ADDRESSEE: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSILAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07063
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05058
 FILING DATE: Concurrently
 CLASSIFICATION:
 APPLICATION NUMBER:

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FILING DATE: ;
ATTORNEY/AGENT INFORMATION: ;
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-255
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05058-2

Query Match Best Local Similarity 100.0%; Score 1578; DB 1; Length 283;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDWGPWRSPTRPTDVLRLVLYLPIGACYAPALPSCKEDEVVGSECCPKCSPG 60
Db 1 YRVKEACGELGTGTVCECPGTYIAHNLGSKLCLOQCMCDPAMGLRASRNCSRTEAVCG 120
QY 61 YRVKEACGELGTGTVCECPGTYIAHNLGSKLCLOQCMCDPAMGLRASRNCSRTEAVCG 120
Db 121 CSPGHFCIVQDGHCACRAYATSSPGQRVKGGTESQDTLCNCCPGTFSPNGTLERCO 180
QY 121 CSPGHFCIVQDGHCACRAYATSSPGQRVKGGTESQDTLCNCCPGTFSPNGTLERCO 180
Db 121 CSPGHFCIVQDGHCACRAYATSSPGQRVKGGTESQDTLCNCCPGTFSPNGTLERCO 180
QY 181 HQTKCSWLVTKAGGTSSHHWWFLSSLVIVCSTVGLITCVKURKPRGVKIVS 240
Db 181 HQTKCSWLVTKAGGTSSHHWWFLSSLVIVCSTVGLITCVKURKPRGVKIVS 240
QY 241 VORKRQEAEGETVIEALQAPPDVTTAVEETIPSFGRSRPNH 283
Db 241 VORKRQEAEGETVIEALQAPPDVTTAVEETIPSFGRSRPNH 283

RESULT 5 PCT-US99-20180-13
; Sequence 13, Application PC/TUS9920180
; GENERAL INFORMATION:
; APPLICANT: Millennium Biotherapeutics, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 094/04/079W01
; CURRENT APPLICATION NUMBER: PCT/US99/20180
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: US 09/342,767
; EARLIER FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 09/146,950
; EARLIER FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: SIGNAL
; LOCATION: (1)...(38)
PCT-US99-20180-13

Query Match Best Local Similarity 100.0%; Score 1578; DB 8; Length 283;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDWGPWRSPTRPTDVLRLVLYLPIGACYAPALPSCKEDEVVGSECCPKCSPG 60
Db 1 MEPPGDWGPWRSPTRPTDVLRLVLYLPIGACYAPALPSCKEDEVVGSECCPKCSPG 60
QY 61 YRVKEACGELGTGTVCECPGTYIAHNLGSKLCLOQCMCDPAMGLRASRNCSRTEAVCG 120
Db 61 YRVKEACGELGTGTVCECPGTYIAHNLGSKLCLOQCMCDPAMGLRASRNCSRTEAVCG 120

RESULT 7 US-08-462-962-2

SEQUENCE 2, Application US/08462962

GENERAL INFORMATION:

APPLICANT: NI ET AL.

TITLE OF INVENTION: Tumor Necrosis Factor Receptors

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEES: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05058

FILING DATE: June 5, 1995

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-422

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 283 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-462-962-2

Query Match 100.0%; Score 1578; DB 8; Length 283;

Best Local Similarity 100.0%; Pred. No. 7.2e-19;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDWGPWRSPTRDVLRLVLYLTLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60

Db 1 MEPGDWGPWRSPTRDVLRLVLYLTLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60

QY 61 YRKVEAGGLTGIVCECPGTYIAHLNGLSKLCQCMDPAMGLRASRNCSRTEMAVCG 120

Db 61 YRKVEAGGLTGIVCECPGTYIAHLNGLSKLCQCMDPAMGLRASRNCSRTEMAVCG 120

QY 121 CSPGHFCIVQDGDHACACRAYATSSPGQRVKGGTESQDTLCONCPGPTSPNLTLEBCQ 180

Db 121 CSPGHFCIVQDGDHACACRAYATSSPGQRVKGGTESQDTLCONCPGPTSPNLTLEBCQ 180

QY 181 HOTKCSMLVTKAGTSSHHWWPLSGSLVIVIVCSTVGLLICVRKRKGPRGVVKIVS 240

Db 181 HOTKCSMLVTKAGTSSHHWWPLSGSLVIVIVCSTVGLLICVRKRKGPRGVVKIVS 240

QY 241 VORKRQEAEQGATVIEALQAPPDVTTVAEEETIPSFTGRSPNH 283

Db 241 VORKRQEAEQGATVIEALQAPPDVTTVAEEETIPSFTGRSPNH 283

RESULT 8 US-08-464-595-2

SEQUENCE 2, Application US/08464595

GENERAL INFORMATION:

APPLICANT: JIAN NI, REINER GENTZ AND CRAIG ROSEN

TITLE OF INVENTION: Tumor Necrosis Factor Receptors

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEES: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,595

FILING DATE: June 5, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05058

FILING DATE: April 27, 1995

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-375

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 283 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-464-595-2

Query Match 100.0%; Score 1578; DB 8; Length 283;

Best Local Similarity 100.0%; Pred. No. 7.2e-19;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPGDWGPWRSPTRDVLRLVLYLTLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60

Db 1 MEPGDWGPWRSPTRDVLRLVLYLTLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60

QY 61 YRKVEAGGLTGIVCECPGTYIAHLNGLSKLCQCMDPAMGLRASRNCSRTEMAVCG 120

Db 61 YRKVEAGGLTGIVCECPGTYIAHLNGLSKLCQCMDPAMGLRASRNCSRTEMAVCG 120

QY 121 CSPGHFCIVQDGDHACACRAYATSSPGQRVKGGTESQDTLCONCPGPTSPNLTLEBCQ 180

Db 121 CSPGHFCIVQDGDHACACRAYATSSPGQRVKGGTESQDTLCONCPGPTSPNLTLEBCQ 180

QY 181 HOTKCSMLVTKAGTSSHHWWPLSGSLVIVIVCSTVGLLICVRKRKGPRGVVKIVS 240

Db 181 HOTKCSMLVTKAGTSSHHWWPLSGSLVIVIVCSTVGLLICVRKRKGPRGVVKIVS 240

Db 241 VORKRQEAEGETVIAEQAPPDVTVAEETIPSFTGRSPNH 283
 RESULT 9
 US-08-741-095B-26
 ; Sequence 26, Application US/08741095B
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Rosen, Craig
 ; APPLICANT: Gantz, Reiner
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like 2
 ; FILE REFERENCE: 1488_0770004
 ; CURRENT APPLICATION NUMBER: US/08/741, 095B
 ; CURRENT FILING DATE: 1996-10-30
 ; PRIORITY APPLICATION NUMBER: US 08/464, 595
 ; PRIORITY FILING DATE: 1995-06-05
 ; PRIORITY APPLICATION NUMBER: US 08/462, 962
 ; PRIORITY FILING DATE: 1995-06-05
 ; PRIORITY APPLICATION NUMBER: US 08/462, 315
 ; PRIORITY FILING DATE: 1995-06-05
 ; PRIORITY APPLICATION NUMBER: PCT/US95/05058
 ; PRIORITY FILING DATE: 1995-04-27
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 26
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-741-095B-26
 Query Match 100.0%; Score 1578; DB 11; Length 283;
 Best Local Similarity 100.0%; Pred. No. 7.2e-119; Mismatches 0; Indels 0; Gaps 0;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEPPGDMGPPWRSPTRDVLRLVLYLFLGAPCYAPALPSCKEDEPVGSECCPKCSPG 60
 Db 1 MEPPGDMGPPWRSPTRDVLRLVLYLFLGAPCYAPALPSCKEDEPVGSECCPKCSPG 60
 Qy 61 YRVKEAGELGTQTCVCPGTYIAHNGLISKLCQOCMCDPAMGLRASRNCSRTEAVCG 120
 Db 61 YRVKEAGELGTQTCVCPGTYIAHNGLISKLCQOCMCDPAMGLRASRNCSRTEAVCG 120
 Qy 121 CSPGHFCIVQGDHCAACRAYATSSHHWWFLSGSLVIVIVESTVGLICVVKRKPQGDVVKIVS 180
 Db 121 CSPGHFCIVQGDHCAACRAYATSSHHWWFLSGSLVIVIVESTVGLICVVKRKPQGDVVKIVS 180
 Qy 181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVIVESTVGLICVVKRKPQGDVVKIVS 240
 Db 181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVIVESTVGLICVVKRKPQGDVVKIVS 240
 Qy 241 VORKRQEAEGETVIAEQAPPDVTVAEETIPSFTGRSPNH 283
 Db 241 VORKRQEAEGETVIAEQAPPDVTVAEETIPSFTGRSPNH 283
 RESULT 10
 US-08-987-902-1
 ; Sequence 1, Application US/08987902
 ; GENERAL INFORMATION:
 ; APPLICANT: Avi J. Ashkenazi and Scot A. Marsters
 ; TITLE OF INVENTION: HVEM Polypeptides and Uses Thereof
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Genentech, Inc.
 ; STBBT: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; US-09-342-767-13
 Query Match 100.0%; Score 1578; DB 17; Length 283;
 Best Local Similarity 100.0%; Pred. No. 7.2e-119; Mismatches 0; Indels 0; Gaps 0;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Wipatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/987, 902
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Marschang, Diane L.
 ; REGISTRATION NUMBER: 35,600
 ; REFERENCE/DOCKET NUMBER: PI068R1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5416
 ; FAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 283 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-987-902-1
 Query Match 100.0%; Score 1578; DB 13; Length 283;
 Best Local Similarity 100.0%; Pred. No. 7.2e-119; Mismatches 0; Indels 0; Gaps 0;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEPPGDMGPPWRSPTRDVLRLVLYLFLGAPCYAPALPSCKEDEPVGSECCPKCSPG 60
 Db 1 MEPPGDMGPPWRSPTRDVLRLVLYLFLGAPCYAPALPSCKEDEPVGSECCPKCSPG 60
 Qy 61 YRVKEAGELGTQTCVCPGTYIAHNGLISKLCQOCMCDPAMGLRASRNCSRTEAVCG 120
 Db 61 YRVKEAGELGTQTCVCPGTYIAHNGLISKLCQOCMCDPAMGLRASRNCSRTEAVCG 120
 Qy 121 CSPGHFCIVQGDHCAACRAYATSSHHWWFLSGSLVIVIVESTVGLICVVKRKPQGDVVKIVS 180
 Db 121 CSPGHFCIVQGDHCAACRAYATSSHHWWFLSGSLVIVIVESTVGLICVVKRKPQGDVVKIVS 180
 Qy 181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVIVESTVGLICVVKRKPQGDVVKIVS 240
 Db 181 HOTKCSWLVTKAGACTSSHHWWFLSGSLVIVIVESTVGLICVVKRKPQGDVVKIVS 240
 Qy 241 VORKRQEAEGETVIAEQAPPDVTVAEETIPSFTGRSPNH 283
 Db 241 VORKRQEAEGETVIAEQAPPDVTVAEETIPSFTGRSPNH 283
 RESULT 11
 US-09-342-767-13
 ; Sequence 13, Application US/09342767
 ; GENERAL INFORMATION:
 ; APPLICANT: Busfield, Samantha J.
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE
 ; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: MB1098-061CPL
 ; CURRENT APPLICATION NUMBER: US/09/342, 767
 ; CURRENT FILING DATE: 1999-06-29
 ; EARLIER APPLICATION NUMBER: US 09/146, 950
 ; EARLIER FILING DATE: 1998-09-03
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 13
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(38)
 ; US-09-342-767-13
 Query Match 100.0%; Score 1578; DB 17; Length 283;
 Best Local Similarity 100.0%; Pred. No. 7.2e-119; Mismatches 0; Indels 0; Gaps 0;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
US-09-480-284-1
; Sequence 1, Application US/09480284
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi and Scot A. Masters
TITLE OF INVENTION: hVEM Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/480,284
PRIORITY APPLICATION DATA:
FILING DATE: 10-Jan-2000
PRIORITY APPLICATION NUMBER: US 08/987,902
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1068R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-480-284-1

Query Match 100.0%; Score 1578; DB 18; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119; Length 283;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPGDWGPWRSPRTDVRDLVLYTFLGAPCYAPALPSCKEDEXPVGSBCCPKCSPG 60
Db 1 MPPGDWGPWRSPRTDVRDLVLYTFLGAPCYAPALPSCKEDEXPVGSBCCPKCSPG 60
QY 61 YRVKEAGELGTIVCECPGTYIAHNGLISKLCQCQCDPAMGLRASRNCSRENACG 120
Db 61 YRVKEAGELGTIVCECPGTYIAHNGLISKLCQCQCDPAMGLRASRNCSRENACG 120

QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKGGTESQDTCQNCPPGTSPNGLECO 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKGGTESQDTCQNCPPGTSPNGLECO 180
QY 181 HQTCSWLVTKAGATSSHHWWFLSGSLVIVIVCSTVGLICVKRKPRGDVVKIVS 240
Db 181 HQTCSWLVTKAGATSSHHWWFLSGSLVIVIVCSTVGLICVKRKPRGDVVKIVS 240

QY 241 VORKROEAEGRATVIALQAPPDVTVAVETIPSFTGRSPNH 283
Db 241 VORKROEAEGRATVIALQAPPDVTVAVETIPSFTGRSPNH 283

RESULT 13
US-09-533-262-26
; Sequence 26, Application US/09533262
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like 2
FILE REFERENCE: 148_07000A
CURRENT APPLICATION NUMBER: US/09/533, 262
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: US 60/147, 383
EARLIER FILING DATE: 1999-08-06
EARLIER APPLICATION NUMBER: US 60/135, 169
EARLIER FILING DATE: 1999-05-20
EARLIER APPLICATION NUMBER: US 60/126, 522
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: US 60/125, 683
EARLIER FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 08/741, 095
EARLIER FILING DATE: 1996-10-30
EARLIER APPLICATION NUMBER: US 08/464, 595
EARLIER FILING DATE: 1995-04-27
EARLIER APPLICATION NUMBER: US 08/462, 962
EARLIER FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 08/462, 315
EARLIER FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: PCT/US95/05058
EARLIER FILING DATE: 1995-04-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 26
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-533-262-26

Query Match 100.0%; Score 1578; DB 19; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119; Length 283;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPGDWGPWRSPRTDVRDLVLYTFLGAPCYAPALPSCKEDEXPVGSBCCPKCSPG 60
Db 1 MPPGDWGPWRSPRTDVRDLVLYTFLGAPCYAPALPSCKEDEXPVGSBCCPKCSPG 60
QY 61 YRVKEAGELGTIVCECPGTYIAHNGLISKLCQCQCDPAMGLRASRNCSRENACG 120
Db 61 YRVKEAGELGTIVCECPGTYIAHNGLISKLCQCQCDPAMGLRASRNCSRENACG 120

QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKGGTESQDTCQNCPPGTSPNGLECO 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKGGTESQDTCQNCPPGTSPNGLECO 180
QY 181 HQTCSWLVTKAGATSSHHWWFLSGSLVIVIVCSTVGLICVKRKPRGDVVKIVS 240
Db 181 HQTCSWLVTKAGATSSHHWWFLSGSLVIVIVCSTVGLICVKRKPRGDVVKIVS 240

QY 241 VORKROEAEGRATVIALQAPPDVTVAVETIPSFTGRSPNH 283
Db 241 VORKROEAEGRATVIALQAPPDVTVAVETIPSFTGRSPNH 283


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PRIORITY APPLICATION NUMBER: PCT/US99/12252
PRIORITY FILING DATE: June 2, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/08847
PRIORITY FILING DATE: April 23, 1999
PRIORITY APPLICATION NUMBER: 09/298,404
PRIORITY FILING DATE: April 23, 1999
PRIORITY APPLICATION NUMBER: 09/284,291
PRIORITY FILING DATE: April 12, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/05028
PRIORITY FILING DATE: March 8, 1999
PRIORITY APPLICATION NUMBER: 09/256,311
PRIORITY FILING DATE: March 3, 1999
PRIORITY APPLICATION NUMBER: PCT/US98/00106
PRIORITY FILING DATE: January 5, 1999
PRIORITY APPLICATION NUMBER: 09/218,517
PRIORITY FILING DATE: December 22, 1998
PRIORITY APPLICATION NUMBER: 09/216,021
PRIORITY FILING DATE: December 16, 1998
PRIORITY APPLICATION NUMBER: PCT/US98/25108
PRIORITY FILING DATE: December 1, 1998
PRIORITY APPLICATION NUMBER: PCT/US98/19330
PRIORITY FILING DATE: September 16, 1998
PRIORITY APPLICATION NUMBER: 09/065,275
PRIORITY FILING DATE: April 23, 1998
PRIORITY APPLICATION NUMBER: 08/987,902
PRIORITY FILING DATE: December 10, 1997
PRIORITY APPLICATION NUMBER: PCT/US97/22278
PRIORITY FILING DATE: December 5, 1997
NUMBER OF SEQ ID NOS: 113
SEQ ID NO 46
LENGTH: 283
TYPE: PRT
ORGANISM: Homo Sapien
US-09-882-636-46

Query Match          100.0%; Score 1578; DB 23; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 NEPPGDWGPWRSPTRTDPVRLVLYLTFLGACPAPCYPALPSCKERBYPVGSECCPKCSPG 60
Db      1 NEPPGDWGPWRSPTRTDPVRLVLYLTFLGACPAPCYPALPSCKERBYPVGSECCPKCSPG 60
Qy      61 YRVKEACGELTGTVCPCPPTYIAHNGLISKCLQCQMCIDPAMGLRASRNCSRTENAVCG 120
Db      61 YRVKEACGELTGTVCPCPPTYIAHNGLISKCLQCQMCIDPAMGLRASRNCSRTENAVCG 120
Qy      121 CSPGHFCIVQGDHCACRAYATSSPGQRVYQKGGETSODTICQNCPGTTSPNQGTLBECQ 180
Db      121 CSPGHFCIVQGDHCACRAYATSSPGQRVYQKGGETSODTICQNCPGTFSPNGTLEECQ 180
Qy      181 HOTKCSWLVTAGTSSHHWWFLSGSVLIVTCSTGILICVKRKRRGRGVVKT 240
Db      181 HOTKCSWLVTAGTSSHHWWFLSGSVLIVTCSTGILICVKRKRRGRGVVKT 240
Qy      241 VORKROEAEGEATIVBALQAPPDVTVAVETIPSPFTGRPNH 283
Db      241 VORKROEAEGEATIVBALQAPPDVTVAVETIPSPFTGRPNH 283

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Search completed: November 14, 2003, 17:35:59
Job time : 176 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2003, 17:30:56 ; Search time 20 Seconds

(without alignments)
 683.668 Million cell updates/sec

Title: US-08-741-095B-26
 Perfect score: 1578
 Sequence: 1 MEPPGDMQPPPWRSTPRTDV.....VVIVAVETTIPSFTGRSPNH 283

Scoring table: BLOSUM62
 Gpop 10.0 , Gapext 0.5

Searched: 255527 seqs, 48315734 residues

Total number of hits satisfying chosen parameters: 255527

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_AA_New:*

1: /cgnr2_6/ptodata/1/paa/PCT_NEW_COMBO_PEP:*

2: /cgnr2_6/ptodata/1/paa/US06_NEW_COMBO_PEP:*

3: /cgnr2_6/ptodata/1/paa/US07_NEW_COMBO_PEP:*

4: /cgnr2_6/ptodata/1/paa/US08_NEW_COMBO_PEP:*

5: /cgnr2_6/ptodata/1/paa/US09_NEW_COMBO_PEP:*

6: /cgnr2_6/ptodata/1/paa/US10_NEW_COMBO_PEP:*

7: /cgnr2_6/ptodata/1/paa/US60_NEW_COMBO_PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1578	100.0	283	1 PCT-US02-29560A-288	Sequence 288, APP
2	1575	99.8	283	6 US-10-322-281-546	Sequence 546, APP
3	1575	99.8	283	6 US-10-322-281-548	Sequence 548, APP
4	1575	99.8	283	6 US-10-322-281-550	Sequence 550, APP
5	1575	99.8	283	7 US-60-512-690-303	Sequence 303, APP
6	1575	99.8	283	7 US-60-512-690-304	Sequence 304, APP
7	1575	99.8	283	7 US-60-512-690-305	Sequence 305, APP
8	1575	99.8	283	7 US-60-512-690-306	Sequence 306, APP
9	1477	93.6	282	1 PCT-US03-28227-3157	Sequence 3157, APP
10	1477	93.6	282	1 PCT-US03-28227-3158	Sequence 3158, APP
11	1477	93.6	282	1 PCT-US03-28227-3159	Sequence 3159, APP
12	1477	93.6	282	1 PCT-US03-28227-3160	Sequence 3160, APP
13	1477	93.6	282	1 PCT-US03-28227-3161	Sequence 3161, APP
14	990	62.7	199	7 US-60-512-690-308	Sequence 308, APP
15	787	49.9	172	7 US-60-512-690-307	Sequence 307, APP
16	384.5	24.4	194	6 US-10-322-281-543	Sequence 543, APP
17	267.5	17.0	277	1 PCT-US03-29560A-281	Sequence 281, APP
18	267.5	17.0	277	1 PCT-US03-322-282-28	Sequence 28, APP
19	267.5	17.0	277	5 US-09-467-317-2	Sequence 2, APP
20	267.5	17.0	277	6 US-10-328-953-323	Sequence 323, APP
21	267.5	17.0	277	6 US-10-688-45-28	Sequence 28, APP
22	264.5	16.8	431	1 PCT-US03-28227-3226	Sequence 3226, APP
23	259	16.4	182	4 US-08-484-783B-14	Sequence 14, APP
24	259	16.4	184	4 US-08-484-783B-15	Sequence 15, APP
25	259	16.4	235	4 US-08-484-783B-13	Sequence 13, APP
26	259	16.4	235	5 US-09-882-735A-16	Sequence 16, APP

ALIGNMENTS

RESULT 1
 PCT-US02-29560A-288
 ; Sequence 288, Application PCT/US02/29560A
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Hevezzi, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Wilson, Keith E.
 ; APPLICANT: Zlotnik, Albert
 ; APPLICANT: Bob Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 ; METHODS OF SCREENING FOR MODULATORS OF CANCER
 ; FILE REFERENCE: 018501-002710PC
 ; CURRENT APPLICATION NUMBER: PCT/US02/29560A
 ; CURRENT FILING DATE: 2002-05-17
 ; PRIORITY APPLICATION NUMBER: US 60/323,469
 ; PRIORITY FILING DATE: 2001-09-17
 ; NUMBER OF SEQ ID NOS: 412
 ; SOFTWARE: Fast-SEQ for Windows Version 3.0
 ; SEQ ID NO: 288
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PCT-US02-29560A-288
 ;
 ; Query Match 100.0%; Score 1578; DB 1; Length 283;
 ; Best Local Similarity 100.0%; Pred. No.: 4; Be-5;
 ; Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ; Sequence 3807, APP
 ; Sequence 3808, APP

RESULT 2
US-10-322-281-546
; Sequence 546, Application US/10322281
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 546
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-322-281-546

Query Match 99.8%; Score 1575; DB 6; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55; Mismatches 0; Indels 0; Gaps 0;
Matches 282; Conservative 1; MisMatches 0; Indexes 0;

QY 1 MPPGDWGPWRSTPKTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECPKCSPG 60
Db 1 MEPPGDWGPWRSTPKTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECPKCSPG 60

QY 61 YRKEACGELTGTVCERPPGTYAHNLGSKLCQOCMDPAMGLRASRNCSRTENAVCG 120
Db 61 YRKEACGELTGTVCERPPGTYAHNLGSKLCQOCMDPAMGLRASRNCSRTENAVCG 120

QY 121 CSPGHFCIVQDGHDCAACRAYATSSPGQRVKGGTESQDTLCONCPGPFSPNGTLECO 180
Db 121 CSPGHFCIVQDGHDCAACRAYATSSPGQRVKGGTESQDTLCONCPGPFSPNGTLECO 180

QY 181 HQTKCSMLVTKAGATSSHHWWFLSGSLIVIVCSTVGLIICVRKKPRGVWKIVS 240
Db 181 HQTKCSMLVTKAGATSSHHWWFLSGSLIVIVCSTVGLIICVRKKPRGVWKIVS 240

QY 241 VORKRQEAEATVIEALQAPPDTTVAAVEETIPSFTGRSPNH 283
Db 241 VORKRQEAEATVIEALQAPPDTTVAAVEETIPSFTGRSPNH 283

RESULT 3
US-10-322-281-548
; Sequence 548, Application US/10322281
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 548
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-322-281-550

Query Match 99.8%; Score 1575; DB 6; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55; Mismatches 0; Indels 0; Gaps 0;
Matches 282; Conservative 1; MisMatches 0; Indexes 0;

QY 1 MPPGDWGPWRSTPKTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECPKCSPG 60
Db 1 MEPPGDWGPWRSTPKTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECPKCSPG 60

QY 61 YRKEACGELTGTVCERPPGTYAHNLGSKLCQOCMDPAMGLRASRNCSRTENAVCG 120
Db 61 YRKEACGELTGTVCERPPGTYAHNLGSKLCQOCMDPAMGLRASRNCSRTENAVCG 120

QY 121 CSPGHFCIVQDGHDCAACRAYATSSPGQRVKGGTESQDTLCONCPGPFSPNGTLECO 180
Db 121 CSPGHFCIVQDGHDCAACRAYATSSPGQRVKGGTESQDTLCONCPGPFSPNGTLECO 180

QY 181 HQTKCSMLVTKAGATSSHHWWFLSGSLIVIVCSTVGLIICVRKKPRGVWKIVS 240
Db 181 HQTKCSMLVTKAGATSSHHWWFLSGSLIVIVCSTVGLIICVRKKPRGVWKIVS 240

QY 241 VORKRQEAEATVIEALQAPPDTTVAAVEETIPSFTGRSPNH 283
Db 241 VORKRQEAEATVIEALQAPPDTTVAAVEETIPSFTGRSPNH 283

RESULT 4
US-10-322-281-550
; Sequence 550, Application US/10322281
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-322-281-550

Query Match 99.8%; Score 1575; DB 6; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55; Mismatches 0; Indels 0; Gaps 0;
Matches 282; Conservative 1; MisMatches 0; Indexes 0;

QY 1 MPPGDWGPWRSTPKTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECPKCSPG 60
Db 1 MEPPGDWGPWRSTPKTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECPKCSPG 60

QY 61 YRKEACGELTGTVCERPPGTYAHNLGSKLCQOCMDPAMGLRASRNCSRTENAVCG 120
Db 61 YRKEACGELTGTVCERPPGTYAHNLGSKLCQOCMDPAMGLRASRNCSRTENAVCG 120

QY 121 CSPGHFCIVQDGHDCAACRAYATSSPGQRVKGGTESQDTLCONCPGPFSPNGTLECO 180
Db 121 CSPGHFCIVQDGHDCAACRAYATSSPGQRVKGGTESQDTLCONCPGPFSPNGTLECO 180

QY 181 HQTKCSMLVTKAGATSSHHWWFLSGSLIVIVCSTVGLIICVRKKPRGVWKIVS 240
Db 181 HQTKCSMLVTKAGATSSHHWWFLSGSLIVIVCSTVGLIICVRKKPRGVWKIVS 240

QY 241 VORKRQEAEATVIEALQAPPDTTVAAVEETIPSFTGRSPNH 283
Db 241 VORKRQEAEATVIEALQAPPDTTVAAVEETIPSFTGRSPNH 283

RESULT 5
US-60-512-690-303
; Sequence 303, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aigun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: McCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: CL001478PROV

CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 303
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-512-690-303

Query Match 99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPPGDWGPWPWRSTPKTDVLRLVLYTFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60
Db 1 MEPPGDWGPWPWRSTPKTDVLRLVLYTFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60

Qy 61 YRVKEAGELTGTVCECPGTYIAHNGLSKCOLQCOMCDPAMGLRASRNRSRTENAVCG 120
61 YRVKEAGELTGTVCECPGTYIAHNGLSKCOLQCOMCDPAMGLRASRNRSRTENAVCG 120

Qy 121 CSPGHFCIVQGDHCAACRAYATSSPGQRVKGGTESQDTLCONCPCTPSFGRSNPH 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQRVKGGTESQDTLCONCPCTPSFGRSNPH 180

Qy 181 HOTKCSMLVLTAGAGTSSHHWWFLSGSLVIVCSTVGLICVRKRKRGDVVKIVS 240
181 HOTKCSMLVLTAGAGTSSHHWWFLSGSLVIVCSTVGLICVRKRKRGDVVKIVS 240

Qy 241 VORKROEAEGETVIALQAPPDVTTVAEETIPSFTGRSPNH 283
241 VORKROEAEGETVIALQAPPDVTTVAEETIPSFTGRSPNH 283

RESULT 6
US-60-512-690-304
; Sequence 304, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: C1001478PROV
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 305
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-512-690-305

Query Match 99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPPGDWGPWPWRSTPKTDVLRLVLYTFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60
Db 1 MEPPGDWGPWPWRSTPKTDVLRLVLYTFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60

Qy 61 YRVKEAGELTGTVCECPGTYIAHNGLSKCOLQCOMCDPAMGLRASRNRSRTENAVCG 120
Db 61 YRVKEAGELTGTVCECPGTYIAHNGLSKCOLQCOMCDPAMGLRASRNRSRTENAVCG 120

Qy 121 CSPGHFCIVQGDHCAACRAYATSSPGQRVKGGTESQDTLCONCPCTPSFGRSNPH 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQRVKGGTESQDTLCONCPCTPSFGRSNPH 180

Qy 181 HOTKCSMLVLTAGAGTSSHHWWFLSGSLVIVCSTVGLICVRKRKRGDVVKIVS 240
181 HOTKCSMLVLTAGAGTSSHHWWFLSGSLVIVCSTVGLICVRKRKRGDVVKIVS 240

Qy 241 VORKROEAEGETVIALQAPPDVTTVAEETIPSFTGRSPNH 283
Db 241 VORKROEAEGETVIALQAPPDVTTVAEETIPSFTGRSPNH 283

RESULT 7
US-60-512-690-305
; Sequence 305, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1001478PROV
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 305
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-512-690-306

Query Match 99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPPGDWGPWPWRSTPKTDVLRLVLYTFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60
Db 1 MEPPGDWGPWPWRSTPKTDVLRLVLYTFLGAPCYAPALPSCKEDEVPGSBCCPKCSPG 60

Qy 61 YRVKEAGELTGTVCECPGTYIAHNGLSKCOLQCOMCDPAMGLRASRNRSRTENAVCG 120
Db 61 YRVKEAGELTGTVCECPGTYIAHNGLSKCOLQCOMCDPAMGLRASRNRSRTENAVCG 120

Qy 121 CSPGHFCIVQGDHCAACRAYATSSPGQRVKGGTESQDTLCONCPCTPSFGRSNPH 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQRVKGGTESQDTLCONCPCTPSFGRSNPH 180

Qy 181 HOTKCSMLVLTAGAGTSSHHWWFLSGSLVIVCSTVGLICVRKRKRGDVVKIVS 240
181 HOTKCSMLVLTAGAGTSSHHWWFLSGSLVIVCSTVGLICVRKRKRGDVVKIVS 240

Qy 241 VORKROEAEGETVIALQAPPDVTTVAEETIPSFTGRSPNH 283
Db 241 VORKROEAEGETVIALQAPPDVTTVAEETIPSFTGRSPNH 283

RESULT 8
US-60-512-690-306
; Sequence 306, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES

Best Local Similarity 99.2%; Pred. No. 3.8e-51; Mismatches 1; Indels 0; Gaps 0; Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0; PCT-US03-28227-3161

RESULT 13
PCT-US03-28227-3161
; Sequence 3161, Application PC/TUS0328227
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
; APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
; APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
; APPLICANT: HARTSHORNE, Toinette A.; SUCHOROWSKI, Martin;
; APPLICANT: ALUTIS, Christina M.; PITTS, Steven J.;
; APPLICANT: ELDER, Linda V.; MONEY, Elizabeth M.;
; APPLICANT: DEBEGEANE, Angelo M.; PANESAR, Iqbal S.;
; APPLICANT: BANTVILLE, Steven C.; REDDY, Thirupathan P.;
; APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
; APPLICANT: PANZER, Scott R.; WANG, Xinhao;
; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
; APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
; APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
; APPLICANT: WU, Minghan C.; SUUVE, Laura L.;
; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
; APPLICANT: VITTI, Ursula A.; KIRTON, Edward;
; APPLICANT: XU, Yuning; KWONG, Mary;
; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
; APPLICANT: MA, Yan; JACKSON, Jennifer L.;
; APPLICANT: GRETZEN, Darryl; PATURY, Srikanth;
; APPLICANT: SHI, Xiaobing; SUREZ, Charlyn J.;
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PN-0100 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/28227
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/410,260
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/410,259
; NUMBER OF SEQ ID NOS: 5444
; SOFTWARE: PERL program
; SEQ ID NO 3161
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 928524.PT146P

RESULT 14
US-60-512-690-308
; Sequence 308, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Ai-qun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: McCAFFERY, Ian
; APPLICANT: NARAIN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1001478R07
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-512-690-308

Query Match 62.7%; Score 990; DB 7; Length 199;
Best Local Similarity 100.0%; Pred. No. 2e-32; Mismatches 0; Indels 0; Gaps 0; Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0; PCT-US03-28227-3161

RESULT 15
US-60-512-690-307
; Sequence 307, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Ai-qun

Qy 1 MERPGDWGPPWRSTTRTPDVLVLYLTFLGACYPAPALPSCKEDEPVGSCCPKSPG 60
Db 1 MERPGDWGPPWRSTTRTPDVLVLYLTFLGACYPAPALPSCKEDEPVGSCCPKSPG 60
Qy 1 MERPGDWGPPWRSTTRTPDVLVLYLTFLGACYPAPALPSCKEDEPVGSCCPKSPG 60
Db 1 MERPGDWGPPWRSTTRTPDVLVLYLTFLGACYPAPALPSCKEDEPVGSCCPKSPG 60
Qy 61 YRVKEACGELGTGTVCBPCPPGTYIAHNGSKLCLOQCMCDPAMGLRASRNCSRTENAVCG 120
Db 61 YRVKEACGELGTGTVCBPCPPGTYIAHNGSKLCLOQCMCDPAMGLRASRNCSRTENAVCG 120
Qy 61 YRVKEACGELGTGTVCBPCPPGTYIAHNGSKLCLOQCMCDPAMGLRASRNCSRTENAVCG 120
Db 61 YRVKEACGELGTGTVCBPCPPGTYIAHNGSKLCLOQCMCDPAMGLRASRNCSRTENAVCG 120
Qy 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKQGGTESQDTLCQNCPGTFSPNGTLEBCQ 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKQGGTESQDTLCQNCPGTFSPNGTLEBCQ 180
Qy 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKQGGTESQDTLCQNCPGTFSPNGTLEBCQ 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVKQGGTESQDTLCQNCPGTFSPNGTLEBCQ 180
Qy 181 HOTKCSMLVTKAGATSSHHWWFGLSSLVIVCSTVGLICVKRKPRGDWKIVS 240
Db 181 HOTKCSMLVTKAGATSSHHWWFGLSSLVIVCSTVGLICVKRKPRGDWKIVS 240
Qy 181 HOTKCSMLVTKAGATSSHHWWFGLSSLVIVCSTVGLICVKRKPRGDWKIVS 240
Db 181 HOTKCSMLVTKAGATSSHHWWFGLSSLVIVCSTVGLICVKRKPRGDWKIVS 240
Qy 241 VORKRQEAEGETVIALQAPPDT 265
Db 241 VORKRQEAEGETVIALQAPPDT 265
Qy 241 VORKRQEAEGETVIALQAPPDT 265
Db 241 VORKRQEAEGETVIALQAPPDT 265

; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: CL001478PROV
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 307
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-512-690-307

Query Match 49.9%; Score 787; DB 7; Length 172;
Best local Similarity 99.3%; Pred No. 1.2e-24; Mismatches 1; Indels 0; Gaps 0;
Matches 143; Conservative 0; Mi matches 0; Oy
101 PAMGRASRNCRSRTERENAVCGCSPGHFCYQDGDIACACRAYAASSPGQRVKQGKTESDT 160
Db 17 PAMGRASRNCRSRTERENAVCGCSPGHFCYQDGDIACACRAYAASSPGQRVKQGKTESDT 76
Oy 161 LCQNCPGPSPNGTLECOHQTKCSWLYTKAGACTSSSHWWFLSGSLIVIVVCSTVG 220
Db 77 LCQNCPGPSPNGTLECOHQTKCSWLYTKAGACTSSSHWWFLSGSLIVIVVCSTVG 136
Oy 221 LIICVKRRKERRQDVKVIVSVORK 244
Db 137 LIICVKRRKERRQDVKVIVSVQAK 160

Search completed: November 14, 2003, 17:36:32
Job time : 21 secs

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N

27. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like 2 protein comprising amino acids 1 to 245 of SEQ ID NO:26.
28. The isolated protein of claim 27, which comprises amino acids -38 to 245 of SEQ ID NO:26.
29. The isolated protein of claim 27, which is produced by a recombinant host cell.
30. The isolated protein of claim 27, which comprises a heterologous polypeptide.
31. The isolated protein of claim 30, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
32. (amended) A composition comprising the isolated protein of claim 33 and a carrier.
33. (amended) An isolated protein comprising 30 contiguous amino acids of the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059, wherein said 30 contiguous amino acids comprises an antigenic determinant for the polypeptide consisting of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.
34. The isolated protein of claim 33, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.
35. The isolated protein of claim 33, which is produced by a recombinant host cell.
36. The isolated protein of claim 33, which comprises a heterologous polypeptide.
37. The isolated protein of claim 36, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
38. (amended) A composition comprising the isolated protein of claim 33 and a carrier.
45. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like 2 protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.
46. The isolated protein of claim 45, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.
47. The isolated protein of claim 45, which is produced by a recombinant host cell.
48. The isolated protein of claim 45, which comprises a heterologous polypeptide.
49. The isolated protein of claim 48, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
50. (amended) A composition comprising the isolated protein of claim 45 and a carrier.
57. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like 2 protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

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58. The isolated protein of claim 57, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

59. The isolated protein of claim 57, which is produced by a recombinant host cell.

60. The isolated protein of claim 57, which comprises a heterologous polypeptide.

61. The isolated protein of claim 60, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

62. (amended) A composition comprising the isolated protein of claim 57 and a carrier.

81. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like 2 protein comprising amino acids 1 to 162 of SEQ ID NO:26.

82. The isolated protein of claim 81, which comprises amino acids -38 to 162 of SEQ ID NO:26.

176. (new) The isolated protein of claim 175, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.

host cell.

177. (new) The isolated protein of claim 175, which is produced by a recombinant host cell.

83. The isolated protein of claim 81, which is produced by a recombinant host cell.

178. (new) The isolated protein of claim 175, which comprises a heterologous polypeptide.

84. The isolated protein of claim 81, which comprises a heterologous polypeptide.

179. (new) The isolated protein of claim 178, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

85. The isolated protein of claim 84, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

180. (new) A composition comprising the isolated protein of claim 175 and a carrier.

carrier.

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complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057, wherein said 30 contiguous amino acids comprises an antigenic determinant or the polypeptide consisting of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

polypeptide consisting of the amino acid sequence of SEQ ID NO: 26, wherein said 30 contiguous amino acids comprises an antigenic determinant for the polypeptide consisting of the amino acid sequence of SEQ ID NO: 26.

182. (new) The isolated protein of claim 181, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 17057.

188. (new) The isolated protein of claim 187, which is produced by a recombinant host cell.

183. (new) The isolated protein of claim 181, which is produced by a recombinant host cell.

189. (new) The isolated protein of claim 187, which comprises a heterologous polypeptide.

184. (new) The isolated protein of claim 181, which comprises a heterologous polypeptide.

190. (new) The isolated protein of claim 189, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

191. (new) A composition comprising the isolated protein of claim 187 and a carrier.

185. (new) The isolated protein of claim 184, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

192. (new) An isolated protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.

186. (new) A composition comprising the isolated protein of claim 181 and a carrier.

193. (new) The isolated protein of claim 192, which is produced by a recombinant host cell.

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194. (new) The isolated protein of claim 192, which comprises a heterologous polypeptide.

195. (new) The isolated protein of claim 194, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

196. (new) A composition comprising the isolated protein of claim 192 and a carrier.

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41. (amended) An isolated antibody which specifically binds to a polypeptide consisting of amino acids -38 to 245 of SEQ ID No. 26.

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N

62. (New) A hybridoma which produces the monoclonal antibody of claim 42.

42. (Once amended) The isolated antibody of claim 41, wherein said antibody is monoclonal antibody.

43. (Once amended) The isolated antibody of claim 41, wherein said antibody is oligoclonal antibody.

44. (Once amended) The isolated antibody of claim 41, wherein said antibody is chimeric antibody.

45. (Once amended) The isolated antibody of claim 41, wherein said antibody is humanized antibody.

46. (Once amended) The isolated antibody of claim 41, wherein said antibody is single-chain Fv antibody.

47. (Once amended) The isolated antibody of claim 41, wherein said antibody is Fab antibody fragment.

A composition comprising the Ab of claim 41 and a pharmaceutically acceptable carrier.

60. (New) The isolated antibody of claim 41, wherein said antibody is the product of an Fab expression library.

61. (amended) A method of producing the isolated antibody of claim 41, comprising immunizing an animal with a polypeptide comprising amino acids -38 to 245 of SEQ ID No. and recovering an antibody, which specifically binds, said polypeptide.

63. (New) A method of producing a monoclonal antibody which comprises:
- (a) culturing the hybridoma of claim 62 under appropriate conditions; and

- (b) isolating monoclonal antibody therefrom.

64. (amended) An isolated antibody which specifically binds to a polypeptide consisting of amino acid -38 to 162 of SEQ ID No. 26.

65. (New) The isolated antibody of claim 64, wherein said antibody is a monoclonal antibody.

66. (New) The isolated antibody of claim 64, wherein said antibody is a polyclonal antibody.

67. (New) The isolated antibody of claim 64, wherein said antibody is a chimeric antibody.

68. (New) The isolated antibody of claim 64, wherein said antibody is a humanized antibody.

69. (New) The isolated antibody of claim 64, wherein said antibody is a single-chain Fv antibody.

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100. (allowable) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 90% identical to amino acids 1 to 162 of SEQ ID NO: 26, wherein said polypeptide inhibits T cell proliferation.

187. The polynucleotide of claim 186, wherein the sequence of said amino acid sequence is at least 90% identical to amino acids -38 to 162 of SEQ ID NO:26.

188. A method of producing a vector which comprises inserting the polynucleotide of claim 186 into a vector.

189. A vector comprising the polynucleotide of claim 186.

190. A host cell comprising the polynucleotide of claim 186 operably associated with a heterologous regulatory element.

191. A method of producing a polypeptide which comprises culturing the host cell of claim 190 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

192. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids 1 to 162 of SEQ ID NO: 26, wherein said polypeptide inhibits T cell proliferation.

193. The polynucleotide of claim 192, wherein the sequence of said amino acid sequence is at least 95% identical to amino acids -38 to 162 of SEQ ID NO:26.

194. A method of producing a vector which comprises inserting the polynucleotide of claim 192 into a vector.

195. A vector comprising the polynucleotide of claim 192.

196. A host cell comprising the polynucleotide of claim 192 operably associated with a heterologous regulatory element.

197. A method of producing a polypeptide which comprises culturing the host cell of claim 196 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

198. An isolated polynucleotide comprising a nucleic acid encoding amino acids 1 to 162 of SEQ ID NO:26.

199. The polynucleotide of claim 198, comprising nucleotides 123 to 608 of SEQ ID NO:25.

200. The polynucleotide of claim 198, comprising a nucleic acid encoding amino acids -38 to 162 of SEQ ID NO:26.

201. The polynucleotide of claim 200, comprising nucleotides 9 to 608 of SEQ ID NO:25.

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84. (New) A composition comprising the antibody of claim 76 and a pharmaceutically acceptable carrier.

85. (amended) A method of producing the isolated antibody of claim 76, comprising:

(a) immunizing an animal with a polypeptide comprising amino acids 1 to 162 of SEQ ID No. 26; and

(b) recovering an antibody, which specifically binds, said polypeptide.

86. (New) A hybridoma which produces the monoclonal antibody of claim 77.

87. (New) A method of producing a monoclonal antibody which comprises:

(a) culturing the hybridoma of claim 86 under appropriate conditions; and

(b) isolating monoclonal antibody therefrom.

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70. (New) The isolated antibody of claim 64, wherein said antibody is an Fab antibody fragment.

71. (New) The isolated antibody of claim 64, wherein said antibody is the product of an Fab expression library.

72. (New) A composition comprising the antibody of claim 64 and a pharmaceutically acceptable carrier.

73. (amended) A method of producing the isolated antibody of claim 64, comprising:

(a) immunizing an animal with a polypeptide comprising amino acids -38 to 162 of SEQ ID No.

26; and

(b) recovering an antibody which specifically binds said polypeptide.

74. (New) A hybridoma which produces the monoclonal antibody of claim 65.

75. (New) A method of producing a monoclonal antibody which comprises:

81. (New) The isolated antibody of claim 76, wherein said antibody is a single-chain Fv antibody.

(a) culturing the hybridoma of claim 74 under appropriate conditions; and

(b) isolating monoclonal antibody therefrom.

82. (New) The isolated antibody of claim 76, wherein said antibody is an Fab antibody fragment.

77. (New) The isolated antibody of claim 76, wherein said antibody is a monoclonal antibody.

78. (New) The isolated antibody of claim 76, wherein said antibody is a polyclonal antibody.

76. (amended) An isolated antibody which specifically binds to a polypeptide consisting of amino acids 1 to 162 of SEQ ID No. 26.

83. (New) The isolated antibody of claim 76, wherein said antibody is the product of an Fab expression library.

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202. A method of producing a vector which comprises inserting the polynucleotide of claim 198 into a vector.

203. A vector comprising the polynucleotide of claim 198.

204. A host cell comprising the polynucleotide of claim 198 operably associated with a heterologous regulatory element.

205. A method of producing a polypeptide which comprises culturing the host cell of claim 204 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

206. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 90% identical to amino acids 1 to 245 of SEQ ID NO: 26, wherein said polypeptide stimulates T cell proliferation.

213. The polynucleotide of claim 212, wherein the sequence of said amino sequence is at least 95% identical to amino acids 38 to 245 of SEQ ID NO:26.

214. A method of producing a vector which comprises inserting the polynucleotide of claim 212 into a vector.

215. A vector comprising the polynucleotide of claim 212.

216. A host cell comprising the polynucleotide of claim 212 operably associated with a heterologous regulatory element.

217. A method of producing a polypeptide which comprises culturing the host cell of claim 216 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

209. A vector comprising the polynucleotide of claim 206.

210. A host cell comprising the polynucleotide of claim 206 operably associated with a heterologous regulatory element.

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218. An isolated polynucleotide comprising a nucleic acid encoding amino acids 1 to 245 of SEQ ID NO:26.

219. The polynucleotide of claim 218, comprising nucleotides 123 to 857 of SEQ ID NO:25.

220. The polynucleotide of claim 218, comprising a nucleic acid encoding amino acids -38 to 245 of SEQ ID NO:26.

227. (new) A method of producing a vector which comprises inserting the polynucleotide of claim 226 into a vector.

221. The polynucleotide of claim 220, comprising nucleotides 9 to 857 of SEQ ID NO:25.

222. A method of producing a vector which comprises inserting the polynucleotide of claim 218 into a vector.

228. (new) A vector comprising the polynucleotide of claim 226.

229. (new) A host cell comprising the polynucleotide of claim 226 operably associated with a heterologous regulatory element.

230. (new) A method of producing a polypeptide which comprises culturing the host cell of claim 229 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

223. A vector comprising the polynucleotide of claim 218.

224. A host cell comprising the polynucleotide of claim 218 operably associated with a heterologous regulatory element.

225. A method of producing a polypeptide which comprises culturing the host cell of claim 224 under conditions such that said polypeptide is expressed, and recovering said polypeptide.--

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